Sequence 1, Appli Sequence 5, Appli

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US-08-951-148-6
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Sequence 5, Appli
Sequence 1, Appli
Sequence 175, App
                                                                                           December 8, 2002, 06:02:46; Search time 23.357 Seconds (without alignments) 1325.635 Million cell updates/sec
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Sequence 25, 7
Sequence 4, Ap
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/cgn2_6/ptodata/1/ina/6B_COMB.seq:*
/cgn2_6/ptodata/1/ina/PcIUB_COMB.seq:*
/cgn2_6/ptodata/1/ina/PcIUB_COMB.seq:*
              GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.
                                                                                                                                                                                                                                                                                al number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -09-484-970B-44
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PCT-US92-00018-1
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US-09-018-584A-16
US-09-641-638-294
US-08-719-758-1
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                                                                                                                                                                                                                                                     441362 seqs, 153338381 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                    nucleic search, using sw model
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Gapop 10.0 , Gapext 1.0
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Maximum DB seq length: 2000000000
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Match Length DB
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Perfect score:
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RESULT 3
US-09-010-232-1/c
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Best Local Similarity 68.8%; Pred. No. 0.19;
Matches 44; Conservative 0; Mismatches 20; Indels
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4000 Bell Atlantic Tower, 1717 Arch Stre
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CENERAL INFORMATION:
APPLICANT: Black, Michael T.
APPLICANT: Lawlor, Elizabeth J.
APPLICANT: Lawlor, Elizabeth J.
APPLICANT: Lawlor, Elizabeth J.
TILLE OF INVENTION: No. 6200774el Compounds
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dechert, Price & Rhoads
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
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APPLICATION NUMBER: 60/044,365
FILING DATE: 28-ARR-1997
APPLICATION NUMBER: 60/044,366
FILING DATE: 28-ARR-1997
ATTORNEY/AGENT INFORMATION:
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APPLICATION NUMBER: 60/037,857
FILING DATE: 07-FEB-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; Sequence 5, Application US/09010233
; Patent No. 6200774
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IYPE: nucleic acid
STRANDEDNESS: double
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REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: 215-994-2222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Philadelphia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM CONTONERS OPERATING SYSTEM:
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US-09-010-233-5/c
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GENERAL INFORMATION:
APPLICANT: Charles Kunsch
TILLE OF INVENTION: Streptococcus pneumoniae Polynucleotides and Sequences
NUMBER OF SEQUENCES: 391
CORRESPONDENCE ADDRESS:
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4000 Bell Atlantic Tower, 1717 Arch Stre
                                             GENERAL INFORMATION:
APPLICANI: Black, Michael I.
APPLICANI: Lawlor, Elizabeth J.
APPLICANI: Lewis, Ceri J.
IIILE OF INVENTION: No. 6248557el Compounds
NUMBER OF SEQUENCES: 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 31.7%; Score 32; DB 4;
Best Local Similarity 68.8%; Pred. No. 0.19;
Matches 44; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                      OPERATING SYSTEM: DOS
SCHTWARE: FastSEG for Windows Version 2.0
CURRENI APPLICATION DAIA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/09/010,232 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/937,857
FILING DATE: 07-FEB-1997
APPLICATION NUMBER: 60/044,366
FILING DATE: 28-APR-1997
APPLICATION NUMBER: 60/044,365
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: 60/044,365
FILING DATE: 28-APR-1997
ATIORNEY/AGENT INFORMATION:
Sequence 1, Application US/09010232
Patent No. 6248557
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TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                             IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACIERISTICS:
LENGTH: 300 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                        COUNTRY: USA
ZIP: 19103-2793
COMPUTER READABLE FORM:
MEDIUM IYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Falk, Stephen T
REGISTRATION NUMBER: 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INFORMATION FOR SEG ID NO:
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                                                                                                                                                                                       CORRESPONDENCE ADDRESS: ADDRESSE: Dechert, 1
                                                                                                                                                                                                                                                             Philadelphia
                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM CON
OPERATING SYSTEM:
SOFTWARE: FASTSEC
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US-08-951-527-175/c
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AQ551385 Sheared D
AL514767 AL514767
AQ899744 HS_5234.A
AQ931126 RPCI-23-2
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AL547213 AL54293 AL547213 AL547213 AL547213 AL547213 AL547213 AL547213 AL547213 AL55613 ZM0225002 BH152433 ENTPD447R
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AJ772083 EST253183
AM177332 CM1 CT012
AQ765687 HS_5372_A
BG765662 602734_SS
ALI01367 Droscphil
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BH624692 BACPP20-L
AZ638018 1M0497009
BH634121 BACPP6-K1
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AW177341 CM1-CT012
AW177381 CM4-CT012
AW177379 CM4-CT012
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432 bp mRNA linear ESI 09-NOV-1997
2005011:1 Soares_Lestis_NHT Homo sapiens cDNA clone IMAGE:731051
5/ simicar to gb:X51602_cds1 VASCULAR ENDOTHELIAL GROWTH FACTOR
RECEPTOR 1 (HUMAN); mRNA sequence.
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Hillier,L. Allen,M., Bowles, Catarrhinh; Hominidae; Homo.
Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost,S.,
Krizmar,D., Kucaba,T., Lacy,M., Le,M., Lennon,G., Marra,M., Martin,V.J., Morre,B., Schellenberg,K., Steptoe,M., Ian,F., Ineising,B.,
Wash,D.N.; Mylle,T., Waterston,R. and Wilson,R., Theising,B.,
Wash,D.N.; Inman EST Project
BIB20394 603036284
BH768691 BMBAC361D
AL016000 F.rubripe
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AZ628465 1M0480N05
AG029559 Pan trogl
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A1317199 u135g03.y
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Bukarycia; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Dmail: estewatson.wustl.edu
Mis.ci.de is available royalty-free through LLNL ; contact the
IMAGE Consortium (infodimege.llnl.gov) for further information.
Insert length: 801 Std Error: 0.00
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444 Forest Park Parkway, Box 8501, St. Louis. MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
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BF528560
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BG762662
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AA121341/c
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DEFINITION
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VERSION
KEYWORDS
SOURCE
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AUTHORS
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AQ779483 HS_3001_A
AZ809047 ZM0072E19
BG538053 602563562
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AIÜ25332 OV74903.X
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2086.058 Million cell updates/sec
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                                                                                                   8, 2002, 05:54:07; Search time 784.132 Seconds
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1 atatggtgcctgtggtctcc......tatgtaaatgcttccaagtt 151
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           GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.
                                                                                                                                                                                                                                                                   16154066 seqs, 8097743376 residues
                                                                                                                                                                                                                                                                                              of hits satisfying chosen parameters:
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Maximum Match 1008
Listing first 45 summaries
                                                                      OM nucleic - nucleic search, using sw model
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/lab_host="DH103"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Robert Strausberg, Ph.D. Email* cgapbs-rémail.nih.gov CDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima Bonaido
                                                                                                                                                                                                                        /note="Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I: Site_2: Eco RI; 1st strand cDNA was prepared from mRNA obtained from Clontech Laboratories
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Information can be
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1 (bases 1 to 513)

NCI-CGAP http://www.ncbi.nlm.nih.gov/nciogap.

National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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www.bio.llnl.gov/bbrp/image/image.html
Insert Length: 41 Std Brror: 0.00
Seg primer: -40ml3 fwd. Er from Amersham
High quality sequence stop: 370.
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Pred. No. 6.4e-15;
0; Mismatches 0;
Seq primer: -28ml3 rev2 ET from Amersham
High quality sequence stop: 346.
Location/Qualifiers
                                                                                                                                        /clone="lMAGE:731061"
/clone_lib="Soares_testis_NHT"
/sex="male"
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/db_xref="GDB:5927885"
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/db_xref="taxon:9606"
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KEYWORDS
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AI025332
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/note="Vector: p1713D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA was prepared from mRNA obtained from Clontech Laboratories
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Alonso, J.M., Leisse, T.J., Barajas, P., Chen, H., Cheuk, R., Gadrinab, C., Jeske, A., Karnes, M., Kim, C.J., Parker, H., Preddis, L., Shinn, P., Inmerman, J. and Ecker, J.R.
A Sequence-Indexed Library of Insertion Mutations in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           directly sequenced to determine the genomic sequence at the site of insertion. Details of the protocols used can be found at http://signal.salk.edu/tdna_protocols.html*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Sperimacophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosida II; Brassicales; Brassicaceae; Arabidopsis. ( (bases I to 232)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /clone_lib='Arabidopsis thaliana IDNA insertion lines'
'Arote='PCR was performed on Arabidopsis thaliana lines
each of which contains one or more IDNA insertion
elements. The resultant fragment for each line was
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This is single pass sequence recovered from the left border of IDNA. This sequence lies within 300 bases of the 3' end of At5g05150.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BH757424
SALK_056184.53.00.x Arabidopsis thaliana IDNA insertion lines
Arabidopsis thaliana genomic clone SALK_056184.53.00.x, DNA
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                                                                                                                                                                                                                                                                                                                                                                                                 Length 513;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Salk Institute Genomic Analysis Laboratory (SIDAL)
The Salk Institute for Biological Studies
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
Tal: 858 453 4100 x1752
Fax: 858 558 6379
                                                                                                                                                                                                                                                                                                                                                                                                 Score 74.4; DB 9;
Pred. No. 1.7e-08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Arabidopsis thaliana"
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/clone="SALK_056184.53.00.x"
                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Mismatches
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1. .232
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Alab_marter Devolant National Transistant, France Wester PWb2nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch or filter at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligon.cleotides were ligated to the bluin ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 1.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of plasmid R1. Inc vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse LNA was annealed to adaptored vector DNA, and transformed into
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Rm. 308, Blomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
                                                                A2809647 476 bp DNA linear GSS 20-FEB-2001 2M0672E19R Mouse 10kb plasmid UUGCIM library Mus musculus genomic clone UUGC2M0072E19 R, DNA sequence.
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                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 476)
                                                                                                                                                                                                                                                                                                                     Dunn, D., Aoyagi, A., Barber, M., Beacorn, I., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meanen, E., Federsen, T., Reilly, M., Rose, M., Rose, M., Stokes, R., Tingey, A., von Mederhausern, A. and Wright, D., Weiss, R.
                                                                                                                                                                                                                                                                                                                                                                                                              Mouse whole genome scaffolding with paired end reads from 10kb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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63.0%; Pred. No. 1.8e+02;
tive 0; Mismatches 30; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: ddunn&genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0072 row; E column: 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Seq primer: CACACAGGAAACAGCTATGACC
class: plasmid ends
High quality sequence stop: 476.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
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/clone="UUGC2M0072E19"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            Unpublished (2000)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Tel: 801 585 5606
Fax: 801 585 7177
                                                                                                                                                                                                                                                                                                                                                                                                                                        plasmid inserts
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Best Local Similarity
Matches 51; Conserv
                                                                                                                                                                                                              house mouse.
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                        RESULT 5
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                                                                                                                                                                                                                                                                                                                                                                                           AQ7/9483 508 bp DNA linear GSS 02-AUG-1999 HS_3001_A1_B02_T7C CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3001 Col=3 Row-C, DNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 508)
Mahairas, G.G., Wallace, J.C., Smith, K., Swartzell, S., Holzman, T., Keller, A., Shaker, R., Furlong, J., Young, J., Zhao, S., Adams, M.D. and Hood, L.
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Clones may be purchased from Research Genetics (info@tesgen.com).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /clone_lib="CIT Approved Human Genomic Sperm Library D'
/sex="male"
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                                                                                                                                                                                      6 CTAIGAACTICTGAGAGAACTGAGAAGTITTGCCATTGTTTTTTTTT 65
                                                                                                                                                         10 CTGTGGTCTCCTGACTCATTAGAGCTGGATGCCTTTTCCTGTCTTGAIAATTCTTTCTGT 69
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Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)
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                                                                   Length 232;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           High Throughput Sequencing Center
University of Mashington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
Tel: (206) 616-3618
Fax: (206) 616-3887
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4 others
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Plate: 3001 row: C column: 3
  15 others
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                                                                Score 33.2; DB 17;
Pred. No. 1.7e+02;
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/db_xref="taxon:9606"
/clone="Plate=3001 Col=3 Row=C"
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Location/Qualifiers
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40 g
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Class: BAC ends
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Brudia malayi
Bukaryoda, Merazoa; Nematoda; Chromadorea; Spirurida; Filarloidea;
Onchocercidae: Brugia.
1 (bases 1 to 668)
Whitton, C., Paub,J., Ware,J., Quail,M., Hall,N., Barrell,B., Foster
J., Guillano,D., Slatko,B. did Blaxer,M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BH768651 658 bp DNA linear GSS 20-MAR-2002 BMBAC361D117_PSU Brugia malayi Genomic Bac Library 3 Brugia malayi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="Organ: pooled brain, lung, testis; Vector:
PCMV-SPORT6; Site_1: Not1; Site_2: EccN (destroyed); RNA
source anonymous pool of 6 male brains, age range 23-27; 1
male lung, age 27; and 1 male testis, age 69. Library is
oligo-dT primed and directionally closed (EccNV site is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    destroyed upon cloning). Average insert size 1.8 kb, insert size range 1-3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 021. Note: this is a NHHMGC Library."
                                                  Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                            cDNA Library Preparation: Life Technologies, Inc.
DNA Library Arrayed by: The T.M.A.G.E. Consorthum (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
                                                                                                                          NIH-WGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammallan Gene Collection (MGC)
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http://image.llnl.gov
Plate: LLAM1141 row: h column: 21
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Institute of Cell, Animal and Population Biology
University of Edinburgh
                                                                                                                                                                                                                            Email: cgapbs-rēmail.nih.gov
Tissue Procurement: Life Technologies, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /clone="IMAGE:5177156"
/clone_lib="NIH_MGC_115"
/lab_host="DH10B"
                                                                                                                                                                                                          Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                            High quality sequence stop: 451.
Location/Qualifiers
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                                                                                                                                                                               EST 03-APR-2001
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B1820394
E8820394.1 GI:15931944
                                                                                                                                                                          BG588053 1197 bp mRNA linear EST 03-APR-602863562Fl NIH_MGC_77 Homo sapiens cDNA clone IMAGE:4688391 5'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LINL at:
http://Anage.loll.gov/*
Plate: LICMI502 row: k column: 16
High quality sequence stop: 237.
1. 1197
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: cgapbs-rémail.nih.gov
Tissue Procurement: CLONTECH Laboratories, Inc.
CDNA Library Preparation: CLONTECH Laboracories, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
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/clone_lib="NIH_MGC_77"
/lab_host="DH10B (T1 phage-resistant)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Homo sapiens"
/db_xref="taxon:9606"
                          212 FICCTAPTTCATGATTTA 232
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77 TIAGATATGTAAATGCTTICA 97
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/clone="085H11ac2"
/clone_lib="cosmid 089H11"
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62,8%;
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                                                                  Email: mark.lly.axier.ed.ac.uk
Sequenced from the Brugia malayi BAC library constructed by Claire
Whitton and Dr Mike Quail. The sequence was generated by The
Pathogen Sequencing Unit, The Sanger Institute, Cambridge, UK in
collaboration with Mark Blaxter, ICAPB, University of Edinburgh,
Edinburgh, UK.
Seq primer: T? TAATACGACTCACTATAGGG)
Class: BAC ends.
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Vector: pBluescript II KS
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Actinopterygii, Neopterygii, Teleostei, Buteleostei, Neoteleostei,
Acanthomorpha, Acanthopterygii, Percomorpha, Tetraodontiformes,
Ashworth Labs, King's Buildings, West Mains Road, Edinburgh, EHS
                                                                                                                                                                                                                                                                                                                                                                                 /note="Vector: pBACe3.6; Site_1: BamH I; Brugia malayi
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Williams,G. and Brenner,S.
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                                                                                                                                                                                                                                                                                  /driverser.com:6279"
/clone_lib="Brugia malayi Genomic Bac Library 3"
/sex="Mixed (male and female)"
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                                                                                                                                                                                                                                                                                                                                               /tissue_type="whole parasite"
/dev_stage="microfilaria (L1)"
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/db_xref="taxon:31033"
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/strain="TRS"
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1. .668
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Takifugu rubripes.
Takifugu rubripes
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                                  Tel: +44 131 650 6760
Fax: +44 131 670 5450
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435 bp. mRNA linear EST 18-APR-2002
Yonic inner ear subtracted cDNA Danio
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Eukaryota; Netazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes
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Coimbra,R., Weil,D., Brottier,P., Blanchard,S., Levi,M., Hardelin,J.P., Weissenbach,J. and Perit,C.
A subtracted cDNA library from the zebrafish (Danio rerio)
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Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: segrefägenoscope.cns.fr, Web : www.genoscope.cns.fr.
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Pred. No. 3.9e+02;
0; Mismatches 29; Indels
1 cthers
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                                                           6; DB 17;
4e÷02;
ches 29;
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/dev_stage="embryonic"
/note="subtracted cDNA library"
a 102 c 65 g 125 t
102 t
                                                                                 ed. No. 4e+07
Mismatches
                                                             Score 31.6;
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/clone="BN0AA088ZF04"
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81 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note-"Vector: pUC18; Site_1: Smal; Constructed at The Institute for Genomic Research (TIGR), Rockville, MD. Genomic DA isolated from a cloned population of Trypanosoma brucei (TREU927/4 GUTAT 10.1) was mechanically
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                                                                                                                     1 (bases 1 to 555)
El-Sayed,N., Zhao,S., Zhao,H., Gill,S., Sub,E., Malek,J., Fujii,C.,
Gerrand,C., Leech,V., de Jong,P., Ullu,E., Melville,S., Donelson,J.,
Fraser,C. and Adams,M.
Determination of clone end sequences from Irypanosoma brucei GUIat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequencing projects. In Genome Sequencing: A Practical Approach, eds. M. Vaudin and B. Barell, Oxford University Dress 1960.
                                                                                                                                                                                                                                                                                                                                                                                                             Email: nelsayed@tigr.org
Clones are derived from the Trypanosoma brucei GUTat 10.1 sheared
DNA library constructed at TIGR. Clones will be available for
distribution through ATCC. Sheared DNA end sequences search page:
http://www.iofr.org/idb/mdb/tbdb/.
Seq primer: MI3-Reverse
Class: shotgun.
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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                                                                                  Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
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                                                                                                                                                                                                                                                                                                           Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
etc. 301 838 0200
Fax: 301 838 0208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Trypanosoma brucei"
/strain="TREU927/4 GUTat 10.1"
/db_xref="taxon:5691"
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/clone_lib-"Sheared DNA"
                                                                                                                                                                                                                                              Unpublished (1999)
Other_GSSs: Sheared DNA-17L3.TF
Contact: Najib M. El-Sayed
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83 c
  AQ651385.1 GI:5144571
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Trypanosoma brucei
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/db_xref="taxon:9606"
/clone="clobable2002"
/clone=lib="trl NFL006_PL2"
/tissue_type="placenta"
/tissue_type="placenta"
/ficte="Vector: pCWVSPORT 6; Site_i: Noti; lst strand CDNA was primed with a NoLI-0190(df) primer. Five prime end enriched, double-stranded CDNA was digested with Not I and cioned into the Not I and Eco RV sites of the pcWVSPORT 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          vector. Library was normalized. Library was constructed by Life Technologies. Contact: Feng Ling Life Technologies. Contact: Feng Ling Life Technologies, a division of Invircogen 9800 Medical Center Drive Rockville, Maryland 20856, USA Fax: (1) 301 610 8371 Email: filangalifetech.com URL: http://fulllength.invircogen.com.
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Keller,A., Shaker,R., Furlony,J., Young,J., Zhao,S., Adams,M.D. and
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Clones are derived from the human BAC library RFCI-11. For BAC
library availability, please contact. Pieter de Jong
(pieterédejong.med.buffalo.edu.) Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/ordering_bac.htm)
or from Resear h Genetics (infoéresgen.com). BAC end Web Server:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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BP 191 91006 EVRY cedex – France
Email: segrefêgênoscope.cns.fr, Web : \#ww.genoscope.cns.fr.
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95380589
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Pred. No. 3.8e+02;
6; Mismatches 25; Indels 6
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University of Washington
401 Queen Anne Avenue North, Seattle, WA 98169, USA
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1 (bases 1 to 578)
Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
Full:length cDNA libraries and normalization
Unpublished (2001)
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illarity 58.18;
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Fax: (206) 616-3887
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Query Match
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COMMENT
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                                                                                                                                                                                                                                                        /note="Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI;
Male blood DNA was isolated from one randomly chosen donor
and partially digested with a combination of EcoRI and
EcoRI Methylase. Size selected DNA was cloned into the
pBACe3.6 vector at EcoRI sites?

3. 236 c 140 g 338 t
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RPCI-23-282B4.TJ RPCI-23 Mus musculus genomic clone RPCI-23-282B4,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Zhao,S., Nierman,W., Feldblyum,T., Malek,J., Shatsman,S., Akirret,B., Levins,M., Mogann,S., Tsegaye,G., Geer,K., Krol,M., de Jong,P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: szhaoétigr.org
Clones are derived from the mouse BAC library RFCI-23. FOR BAC
Clones are derived from the mouse BAC library availability, please contact Pieter de Jong
(pleterédejong.med.buffalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/orderingframe.htm)
or from Resea ch Genetics (infoéresgen.com). BAC end page:
http://www.tigr.org/ddb/bac_ends/mouse/bac_end_intro.html
Seq primer. SP6
class: BAC ends.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mammaiia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 554)
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostoml;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 ATATGGIGCCTGTGGTCTCCTGACTCATTAGAGCTGGATGCCTTTTCCTGTCTTGATAAT 60
                                                                                                                                                                                                                                                                                                                                                                                                                                    31.3%; Score 31.6; DB 17; Length 911; 62.8%; Pred. No. 3.7e+02;
                                                                                                                                                                          /clone="place=9002 Col=19 Row=K" /clone lib=RPCI-11 Human Male BAC Library" /sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3712 Medical Center Dr., Rockville, MD 20850, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    and Fraser, C.M.
Mouse BAC End Sequences from Library RPCI-23
Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Department of Eukaryotic Genomics The Institute for Genomic Research
                                                                                                                                                     /organism="Homo sapiens"
                                                                                  High quality sequence stop: 911.
Location/Qualifiers
http://www.htsc.washington.edu
Plate: 9002 row: K column: 19
Seq primer: T7
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Contact: Shaying Zhao
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AQ931126.1 GI:6620140
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Fax: 301 838 0208
                                                                                                                                   116
                                                                     Class: BAC ends
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/organism="Mus musculus"

.554

/db_xref="taxon:10090"

/strain="C57BL/6J

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AW588030 452 bp mRNA linear EST 02-JUN-2000 uf91c01.yl Soares_mammary_gland_NMLMG Mus musculus cDNA clone IMAGE:1529472 5' similar to TR:094636 094636 HYPOTHEICAL PROTEIN;;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note-vector: p1713D-Pac (Pharmacia) with a modified polylinker; lst strand cDNA was prepared from mammary gland tissue from a lactating female, and was then primed with a Not I - oligo(dI) primer. Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified p1713 vector. Library is normalized. Library was constructed by Bento Scares and M. Fatima Bonaldo.
                                                                                                                                                                                                                   selected DNA was cloned into the pBACe3.6 vector at the EcoRI sites. The ligation products were transformed into DH10B electrocompetent cells (BRL Life lechnologies).
                                                                                                                                                                                                                                                                                                                                                                                                                                                           ô
                                                                                                      Anote-*Organ: Kidney/Brain; Vector: pBACe3.6; Site_1:
ECORI; Site_2: ECORI; Female C78H./5J mouse kidney and/or
brain genomic DNA was isolated and partially digested
with a combination of ECORI and ECORI Methylase. Sige
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Lenaryota, Metakoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Banamalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 (bases 1 to 452)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. M31:945572
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                62 CICCICITGIGGIAAAACCICATGCCTTTTTTTCCCTTTGFAAITCITICITTCTTTTA 121
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o
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Pred. No. 4.3e-02;
0; Mismatches 31; Indels 0;
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Pred. No. 4.9e+02;
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/tissue_type="mammary gland"
/lat_host="DH108"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism-"Mus musculus"
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/clone="IMAGE:1529472"
/clone="RPCI-23-282B4"
/clone_lib="RPCI-23"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: cgapbs-r@mail.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Seq primer: -40RP from Gibco
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                                                                                 /lab_host="DH10B"
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nilarity 61.7%;
Conservative 0,
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                                                   /sex="Female"
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0; Gaps 0; Mismatches 34; Indels Astrohes 51; Conservative

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Pubpna/USO7_NEW_PUB.seq:*
Pubpna/PCTUS_PUBCOMB.seq:
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/ptodata/1/pubpna/US08_PUBCOMB.seq:
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GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.
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/cgn2_6/ptodata/1/pubpna/PCT_
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Maximum Match 100%
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Gapop 10.0 , Gapext 1.0
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Maximum DB seq length: 200000000
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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Score 32, DB 10; Length 288; Pred. No. 2.2;

31.78;

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3 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4		ESULT 1 S-09-815-142-4447/C. S-09-816-4447, Application US, Patent No. US20020061569A1 GENERAL INCRANION	ICANT:	ICANT: ICANT:	ICANT: ICANT:	E OF INV	ENT PILI	R APPLIC R FILING R APPLIC	R APPLIC	R FILING	OR FILLING OR APPLIC OR FILLING	NR FILING NE FILING NER OF SEC	9036 1408	NESM: 5-242-	
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Query Match 31.7%; Score 32; DB 10; Length 303; Best Local Similarity 68.8%; Pred. No. 2.3; Matches 44; Conservative 0; Mismatches 20; Indels
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                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: Identification of Essential Genes in
TILE OF INVENTION: Prokaryotes
FILE REFERENCE: ELITRA.011A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DAIE: 2000-11-27
PRIOR FILING DAIE: 2000-12-22
PRIOR FILING DAIE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DAIE: 2001-02-16
NUMBER OF SEQ ID NOS: 14110
SCITWARE: FREESEQ for Windows Version 4.0
SEQ ID NO 8767
                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT FILING DATE: 2001.03-21
PRICE APPLICATION NUMBER: 60/2191,078
PRICE APPLICATION NUMBER: 60/206,848
PRICE RING DATE: 2000-05-23
PRICE RING DATE: 2000-05-23
PRICE RING DATE: 2000-05-26
PRICE RING DATE: 2000-05-26
PRICE APPLICATION NUMBER: 60/207,727
PRICE APPLICATION NUMBER: 60/242,578
PRICE FILING DATE: 2000-05-26
PRICE FILING DATE: 2000-05-26
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US-05-101-14
US-05-101-14
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PRIOR FILING DAIE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
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Irawick, John D. Carr, Grant J. Yamamoto, Robert T.
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                                                                                                                                                                                 Carr, Grant J.
Yamamoto, Robert T.
Xu, H. Howard
Chlsen, Kari L. P.
Zyskind, Judith W.
Wall, Daniel
Trawick, John D.
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US-09-815-242-8767
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APPLICANT:
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    0; Gaps
                                                                                 38 AIGCCTITTCCTGTCTTGATAATTCTTTTTTTTTTTTAGATATGTAAATGCTTTCA 97
                                                                                                                                          104 AIGCITICIAATGIGTIGGCCATITCTTCCGTTTCTTCAGGAGAAATITGAAGTCTIGCA 45
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    0; Mismatches 20; Indels
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US-09-815-212-8767/c
Sequence 8767, Application US/09815242
Patent No. US20020061569A1
GENERAL INFORMATION:
APPLICANT: Haselbeck, Robert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; Sequence 8393, Application US/09815242
; Patent No. US20020061569A1
    Matches 44; Conservative
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US-09-815-242-8393
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US-09-815-242-8393/c
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NAME/KEY: CDS
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APPLICANT: Cafferkey, Robert
APPLICANT: Sub. Yongmaing
APPLICANT: Sub. Yongmaing
APPLICANT: Liu, Chenghua
TILE OF INVENTION: Compositions and Methods Relating to Breast Specific Genes and
FILE REFERENCE: DEX-036 F. DEX-036 CURRENT APPLICATION NUMBER US/10/001,887
CURRENT APPLICATION NUMBER US/10-200
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TITLE OF INVENTION: ANTISENSE MODULATION OF PIFIB EXPRESSION
FILE STERENCE: ISPH-0576
CURRENT FILING DATE: 2001-05-14
PRIOR PELICATION NUMBER: US 09/629,644
PRIOR PELICATION NUMBER: US 09/629,644
PRIOR FILING DATE: 2000-07-31
PRIOR FILING DATE: 2000-07-31
PRIOR PELICATION NUMBER: US 09/487,366
PAGE FILING DATE: 2000-01-18
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                                                                                                                                                                             PRICE APPLICATION UNMER: 60/249, 996
PRICE FILING DAIE: 2000-11-20
PRICE APPLICATION NUMBER: 60/252,563
PRICE FILING DAIE: 2000-11-22
NUMBER OF SEQ. ID NOS: 137
SEQ. ID NO 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 243, Application US/09854883 Patent No. US20020055479al GENERAL INFORMATION:
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NAME/KEY: misc_feature
LCGAILON: (231), (231)
OHER INFORMATION: a, c, g or t
NAME/KEY: misc_feature
LCCATION: (245), (246)
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Brett P. Monia
Madeline M. Butler
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Homo sapien
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Best Local Similarity
Matches 52; Conserva
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       APPLICANT:
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Pred. No. 2.3;
0; Mismatches 20; Indels
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F. tent No. US20020107199A1
G. NERAL INFORMATION:
F. TEPLICANT: Walker, Patricia
F. ITLE OF INVENTION: Methods of Administering Botulinum Toxin
F. ILE REFERENCE: 2933CIP
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RIOR FILING DATE: 2000-05-26
RIOR APPLICATION NUMBER: 60/242,578
RIOR FILING DATE: 2000-10-23
RIOR PILING DATE: 2000-11-27
RIOR PLILING DATE: 2000-11-27
RIOR PLLING DATE: 2000-11-27
RIOR APPLICATION NUMBER: 60/257,931
RIOR APPLICATION NUMBER: 60/269,308
RIOR PILING DATE: 2000-12-22
RIOR FILING DATE: 2001-02-16
RIOR FILING DATE: 2001-02-16
RIOR FILING DAIE: 2001-02-16
RIOR FILING DAIE: 2001-02-16
RIOR FILING DAIE: 2001-02-16
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URRENT FILING DATE: 2002-01-17
RIOR APPLICATION NUMBER: 09/730,237
RIOR FILING DATE: 2000-12-05
UMBER OF SEQ. ID NOS: 12
OFTWARE: Patentin Ver. 2.1
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                                                                                                                                                                                                                                                                                                            FYPE: DNA
ORGANISM: Staphylococcus aureus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     31.7%;
68.8%;
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9-815-242-8943
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US-.0-051-952-5/c
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US- 0-001-887-73
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                                                                                                                                                 35 TGGAIGCCITITCCTGTCTTGATAATTCTTTCTGTTTCTTCATIAGAIATGTAAATGCTT 94
                                                                                                                                                                                           10 TGCAITITGIIITCIIITITGATAIITITAIGCCTTCAITITAAAAAIGIAAAICTT 69
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US-09-880-107-3949
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Length 380;
                                                                        20; Indels
Score 28; DB 10;
Pred. No. 29;
0; Mismatches 20;
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US-09-880-107-3545/c
Sequence 3949, Application US/09880107
Patent No. US20020142981A1
GENERAL INFORMATION:
APPLICANT: Horne, Darci T.
APPLICANT: Vockley, Joseph G.
THE TANN: Scherf, UNE
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PRICR APPLICATION NUMBER: EP 00103844.7
NUMBER OF SEQ ID NOS: 2
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 2
LENGTH: 5000
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66.78;
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Best Local Similarity 63.2%;
Matches 43; Conservative (
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Best Local Similarity 63.23
Matches 43; Conservative
                                                                        Conservative
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US-09:791-105-2
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   Query Match
Best Local Similarity
Matches 40; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID FROBES USEFUL FOR
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE BY MICROARRAY
FILE REPERENCE: AGOMICA "X-1
   Db. 47637 CTTIGTTCTGCTGATTGATTACAGCTTGTATATATCTCCATATTTCTAAGCAAAAIGIII 47696
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OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 0.97
OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.1
OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 0.8
OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 0.95
OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 0.95
US-09-664-761-10713
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SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
SEQ ID NO 10713
                                                                                                                   DD 47657 ATCITITIAAAITTAIAAAITCITITATI 47727
                                                                        70 ITCTICATTAGATATGTAAATGCTTTCAAGT 100
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CURRENT FILING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: US 60/180,312
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APPLICATION NUMBER: PCT/US01/00666
FILING DATE: 2001-01-30
APPLICATION NUMBER: PCT/US01/00667
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APPLICATION NUMBER: PCT/US01/00665
FILING DATE: 2001-01-30
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APPLICATION NUMBER: PCT/USO1/00663
TITING DATE: 2001-01-30
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FILING DATE: 2001-01-30
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PRIOR FILING DATE: 2000-09-21
PRIOR APPLICATION NUMBER: US 09/608,408
PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: US 09/774,203
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PRIOR APPLICATION NUMBER: US 60/207,456
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PILING DATE: 2000-08-03
FILING DATE: 2000-08-03
APPLICATION NUMBER: GB 24263.6
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APPLICATION NUMBER: US 60/236,359
                                                                                                                                                                                                                                                                                                                              Sequence 10713, Application US/09864761 Patent No. US20020048763A1 GENERAL INFORMATION: APPLICANT: Penn, Sharron G. APPLICANT: Rank, David R. APPLICANT: Hanzel, David K.
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US-09-864-761-10713
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APPLICANT: ZHANG, HONGYU et al.

TILE OF INVENTION: ISOLATED HUMAN IRANSPORTER PROTEINS,

TILLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN IRANSPORTER PROTEINS,

TILLE OF INVENTION: AND USES THEREOF

FILE REFERENCE: CLOUITZ

CURRENT APPLICATION NUMBER: US/09/813,320
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Gaps
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SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 1695
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US-09-764-564-1695
Sequence 1695, Application US/09764864
Sequence 1695, Application US/09764864
Sevence 1695, Application US/09764864
GENERAL INFORMATION:
SENERAL INFORMATION:
TILLE US INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REPRENCE: P1223
CURRENT APPLICATION NUMBER: US/09/764,864
CURRENT FILING DATE: 2001-01-17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LCCARION: (1)...(397658)
OIMER, INFORMATION: n = A, I, C or G
                                                                                                                                                                        Sequence 3, Application US/09813320 Patent No. US20020142378A1
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) ORGANISM: Homo sapiens
US-09-764-864-1695
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                                      99 GIT 101
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Best Local Si
Matches 55;
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TITLE OF INVENTION: ISOLATED HUMAN TRANSPORTER FROTEINS,

TITLE OF INVENTION: UNCLEIC ACID MOLECULES ENCODING HUMAN TRANSPORTER PROTEINS,

TITLE OF INVENTION: AND USES THEREOF

TILE REFERENCE: CL001172
                      39 IGCCITITCCTGTCTTGATAATTCTTTCTGTTTCATTAGATAGGTTTCAA 98
11 TGTGGTCTCCTGACTCATTAGAGCTGGGTTTTTCCTGICTTGAIAAITCTTTCTGII 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          27.7%; Score 28; DB 10; Length 397658; 77.3%; Pred. No. 1.1e+02;
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                                                                                                                                                                                                                                                                                                                                                             PRIOR FILING DATE: 1999-10-18
PRIOR APPLICATION NUMBER: US09/178,973
FRIOR FILING DATE: 1998-10-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; Sequence 25, Application US/09751797
; Fatent No. US20010024652A1
; GINERAL INFORMATION:
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US- 5-813-320-3
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Schence 3, Application US/09813320
Extenc No. US20020142378A1
G:NERAL INFORMATION:
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Est Local Similarity
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LENGTH: 4797
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US- 9-751-797-25
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Db 1656 TGAT 1659

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RESULT 15
19-09-742-312-3/C
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Search completed: December 8, 2002, 09:29:51 Job time: 274.632 secs

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December 8, 2002, 07:52:47; Search time 5277.36 Seconds (without alignments) 11586.276 Million cell updates/sec
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2101
1 TATATCACAGATGTGCCAAA.......CGACAGCAGCACTCTGTTGG 2101
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copyright (c) 1993 - 2002 Compugen Ltd.
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Maximum Match 100%
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is the number of results predicted by chance to have a Pred. No.

Eukaryota: Metazoa: Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota: Butheria: Primates; Catarrhini; Hominidae: Homo. In teases 1 to 7680)
Shibuya.M.
Direct Submission
Submitted (02-JAN-1989) Shibuya M., Institute of Medical Science, Submitted

REFERENCE AUTHORS TITLE JOURNAL

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

scription	AX51602 Human filt m AX481481 Sequence AF055675 Homo sapi DD8498 Rat mRNA LU7297 Mus musculu NB8689 Mus musculu X78568 Mus musculus AB05372 Gallus ga AJ31588 Homo sapi AC104439 Homo sapi AX481480 Sequence AR201382 Sequence AR201382 Sequence AR201382 Sequence AR201382 Sequence AR0313739 Sequence AR035121 Homo sapi X56165 H.sapies miscul AR040758 Sequence AR030758 Sequence AR030758 Sequence AR030759 Sequence AR030759 Sequence AR05213 Sequence AR05213 Sequence AR05213 Sequence AR05213 Sequence AR05213 Sequence AR05213 Sequence I25171 Seque	A linear PRI 15-NCV-1993 rosine kinase. gene; tyrosine kinase. ; Vertebrata; Euteleostomi;
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Han.H.J., Fujiwara,I., Shin,S. and Nakamura,Y.

Dinucleotide repeat polymorphism in the 3' non-coding region of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AGOTHHOCREBAHWSLDEMVERSELSITKSACGRAGGCSTLINTAQAHH
GFYSCKYLAVPISKKETEBAITFISDTGFFPVENSEIPETHMETERILYITERQAHH
SFNITVILKKFPLDTLIPDGKRINDSRKGFISNAIYRETGLLICEATWGHLYKI
YYLTHROTHILDVOISTFRPWKLIRGHILVUNCTAITPLNIRVQHTWSFPERKREN
SVRRIDQSNSHAFFESKLIDKMONKDKGITCRRRSPSEKKNISVHISVHIYK
TVKRRQOVLETVAGKRSYRLSMKVKAPPSFPVWKLDGIPATEKSRYLIRSYSII
KDYTEEDGANTILLSTRQSNVFKNITAILLYNVKPQIPEKAVSFPDBALYPIGSRO
MALIEGKNWASTLVVADSRIGGITCLASSKYGTVGRUST
                                                                            Nucleotide sequence and expression of a novel human receptor-type tyrosine kinase gene (flt) closely related to the fms family Oncogene 5 (4), 519-524 (1990)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PIEGEDLKLGCTVVRKELYRDVTHILLRTVVRNHYSISOKAAITKEHSITILLIN
NVSLQDSGTYACRARVYTGEELLOKKEIITRDQHAYSLSKOKMAITKEHSITILLIN
HANGVPEPOLIWFKNNHKYQQEPGIILGPGSSTLETERYTEEDEGVYHCKAINGKGSV
ESSATITVQGTSDKSNLELITITGTCVAATLEWILITLIIRKWKSSSSTKIVYLST
MIDDDEVPLDBQCREELVYLSKWEFFARERLKIGKSGAFGKVVQASAFGIKKSFICP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /translation="MVSYMDIGVLLCALLSCLLLIGSSSGSKLKDPELSLKGIQHIMQ
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GNLSNYLKSKROLFFLNKDAALHMEPKKEKMEPGLEGGKKRRILDSVISSESFASGFO
EDKSLSDVEEEEDSDGFYKEPLIMEDLISYSFQVARGMEFLSSRKCIHEDLAAFNILL
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FAELVERLGDLLQANVQODGKDTIPINALITGNSGTYSTPAFSEDFFKESIGAREN
GGSEDDVRYVNAFKFMSLERIKTFEELLPNAISMFDDYQGDSSTLLASPYRETWTD
KFRAGLKIDLRVISKSKESGLSDVSRPSFCHSSCOHVSEGKRETYDHAELEPKIAC
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   of Tokyo, 4-6-1 Shirokane-dai, Minato-ku, Tokyo 108,
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                           Transpared to 7680)
Shibuya.M., Yamaquchi.S., Yamane,A., Ikeda,I., Tojo,A.
Matsushime,H. and Sato,M.
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Location/Qualifiers
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Hum. Mol. Genet. 2 (12), 2204 (1993)
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/db_xref="taxon:9606"
/chromosome="13"
/map="13912"
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/db_xref="G1:31432"
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'note = 1
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                                                                 2260 ACAGTGGCCATCAGAGTTCCACCACTTTAGACTGTCATGCTAATGGTGTCCCGGAGCCT
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                                               AAGGAGCCATCACTATGGAAGATCTGATTCTTACAGTTTCAAGTGCCAGAGGCATG.
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Kreutzer, R., Limmer, S., Rost, S. and Hadwiger, P. Method for inhibiting the expression of a target Patent: WO 02055553-A 95 18-JUL-2002;
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/protein_id="AAC16449.1"
/db_xref="G1:3132831"
/translation="MVSYWDTGVLLCALLSCLL/IGSSSGSKLKDPELSLKGTQHIMQ
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GNLSNYLKSKRDLFFLNKDAALHMEPKKEKMEPGLEOGKKPRLDSVTSSESFASSGFQ
EDKSLSDVEEEEDSDGFYKEPITMEDLISYSFQVARGMEELSSRKCIHPDLAARNILL
SENNYXIODFGLARDIYKNPDYVRKGOTRLPLKHWAPESIFDKIYSTKSDVWSYGVL
LWEIFSLGGSPYPGVQMDEDFCSRLREGMRWRAPEKSTFEIYQIMLDCWHRDPKERPR
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Yu,Y., Whitney,R.G. and Sato.J.D.

Direct Submission
Submitted (06-MAY-1998) Adirondack Biomedical Research Institute,
10 Old Barn Rd., Lake Placid, NY 12946, USA

Location/Qualifiers
3571 GAGGACTICTICAAGGAAAGIAITICAGCTCCGAAGITTAATICAGGAAGCTCTGATGAI 3630
                                           1981 GICAGAIAIGIAAAIGCIIICAAGIICAIGAGCCIGGAAAGAAICAAAACCIIIGAAGAA 2040
                                                                     1 (bases 1 to 4017)
Herley, M.T., Yu, Y., Whitney, R.G. and Sato, J.D.
Characterization of the VESF binding site on the Fit-1 receptor
Blochem. Blophys. Res. Commun. 262 (3), 731-738 (1999)
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receptor: VESF/VPF -binding; Fms/Kit/PDGF receptor family-related;
tyrosine kinase receptor.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (06-FEB-1994) Masabumi Shibuya, Institute of Medical Science, University of Tokyo, Department of Internal Medicine: 4-6-1 Shirokanedai, Minato-ku, Tokyo 108, Japan (Tel:03-5449-5559, Fax:03-5449-5425)
Yamane, A., Seetharam, L., Yamaguchi, S., Gotoh, N., Takahashi, T., Neufeld, G. and Shibuya, M. A new communication system between hepatocytes and sinusoidal endothelial cells in liver through vascular endothelial growth KDR/Fik. 1)

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Oncogene 9 (9), 2683-2690 (1994)
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domain: AA759-780, tyrosine kinase domain: AA813-1152,
kinase insert region: AA930-994."
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Rat mRNA for Fit-1 tyrosine kinase receptor, complete cds.
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/product="fit-1 tyrosine kinase receptor"
/profuctin_id="BAA05857.1"
/db_xref="G1:600379"
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/$train="Fisher F344"
/db.xref="taxon:10116"
/clone="4-4/7-4/3-8"
/tissue_type="lung and testis"
/dev_stage="adult"
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ESSATITYOGTSDKRULELITLICTCVAATLFWLLITEIRKLKRSSEVRIDTLSIT
IVAVEN KEOATSEVRALMTEIKILTHIGHLNVNLLGACTROGGPLMYIVESTTR
ONLSWILKSREDFFCLNKDAALHMEPRKEKLEPDLEDDURDONRENSSESFISSETOR
EDKSVSDVEGGEDVSEISKOPLIMEDLISYSEVRENEDISSESFISSETOR
                                                                                                                                               FAELVEKLGDLLQANVQQDGKDVIPLNAILITRNSGTYSVPTFSEDFFKIGFTDPKTH
SGSEDDVPYVNAFKFMSLERIKTFEELSPNATSMFEDYHLDYSSLLTSFLLKFTWIE
TKPRASMKIDLRIISKSKEAGLSDLPGPSFCFSSCGHIRPVRQEDEDDPELGKESCCS
'SLEDSGIYACRARNIYIGEEILRKTEVLVRDLEAPLLLQNLSDHEVSISGSTT1.DC
                                                                                                               SENNYVKICDFGLARDIYKNPDIVRRGDIRLPLKMAAPBSIFDKVYSIKSDVWSYGVL
LWEIFSLGGSPYPGVQMDEDFCSRLKEGMRMRIPEYAIPBIYQIMLDCWHKDPREPPR
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781 GAGGGGTCCCTIATGATGCAGCAAGTGGGAGTTTGCCGGGAGAGACTTAAACTGGGC 840
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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TGLYTCRYLDTSTSKKKRAESSIYIFVSDAGSPFIEMHTDIPKLVHMFGRGILITPCR
VISPNUTLIKFPPTLILDVGRINDSRRGFILANATYKEIGLLNCEATVNGHLYO
ÄSTIROTNTILDVGIRPSPVRLIHGOTDVLNCTATTELNITVQMSWNTGERATKR
ÄSTROFIDRSHSHNVFHSVLXINNVESRDKGLYTCRVKSGSSFQSFNITVERGF
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KDVITEDAGDYTILLGTKOSELFKULTATLIVWKPQITEKSYSSLPSPILYBLGSR

VALIGTVGIPRPITTWIMHPCHHNISRERYBCTENEESFILDSSRILESTSO

MATHESTRY STLVYADSOTPGITSCRAFUK IGTVERNIKFYTDVBVNGFHYSLES

WPSLEDSGITACRARNIYTGEDILKTTVWNRTHHIGTSKOKMATTQDYSITLALVI

WVSLEDSGITACRARNIYTGEDILKKTEVLYBSEAPHLLONLSDYSTILD
/translation="MVSCRDTAVLPYALLGCLLLTGYGSGSKLKVPELSLKGTQHVMQ
                                                                 1921 GAGGACTICTICAAGGAAAGIATTTCAGCTCCGAAGTTTAAITCAGGAAGCTCTGAFGAI 1980
                                                                                           3807 GAGGACTITITCAAGGAIGGIIICACAGAICCAAAGIIICAITCIGGAAGCICTGAIGAI 3866
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VESAAVLTVOGTSKSNLELITLTCTCVAATLEWILLITERKIKRSSSEVKTDYLSI
MDPDEVPLDEQCERLPYDASKWEFARERLKLGKSLGRGARGKVVQASAFGIKKSPTC
RIVAVKMIKEGAIASEYKALMTELKILIHIGHHLNVVNLLGACTKOGGPLMVIVEYCK
                                                                                                                                                        1981 GICAGAIATGTAAATGCIITCAAGTICAIGAĞCCIGGAAAGAAICAAAACCIITGAAGAA 2040
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SGSSDDVRYVNAFKFMSLERIKIFEELSPNSTSMFEDYOLDTSTLLGSPLLKRFTWTE
IKPKASMKIDLRIASKSKEAGLSDLPRPSFCFSSCGHIRPVQDDESELGKESCCSPPP
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IWEIFSLGGSPYPGVQMDEDFCSRLKEGMRMRIPEYAIPEIYQIMLDGWHKDPKERPR
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receptor protein tyrosine kinase.
Mus.musculus (strain C57BL/63, sub_species domesticus) cDWA to
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/protein_id="AAA40078.1"
/db_xref="GI:293783"
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/db_xref="taxon:10090"
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/strain="C57BL/6J"
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VESAAYLIVOGISDKSNLELITLTCTCVAATLFWLLLTLFIRKLKRSSSEVKTDILSI
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VISPWYYTIKKFPPTLIPDOQRITWDSRAGFIIANAIYKEIGLINCEATVNGHLYQ
YYSPWYYTIKKFPPTLIPDOQRITWDSRAGFIIANAIYKEIGLINCEATVNGHLYG
TMYLIHROIMILIDORDISHWYPERSPYRINUNDSREDKGLYTCRYKSGSSEQSFUSWYPEKGF
ISVKHRKQPVQEIIAGRRSYRLSMXVKAFPSPEIVWLKDGSPAILKSARYLHGYSLI
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                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
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Endothelial growth factor (VEGF) receptor-1 suggests an intimate
evolutionary relationship between the 7-1g and the 5-1g tyrosine
Finnerty, H., Kelleher, K., Morris, G.E., Bean, K., Merberg, D.M., Kitz, R., Morris, J.C., Sookdoo, H., Turner, K.J. and Wood, C.R., Molecular cloning of murine Fit and Fit4 Oncogene 8 (8), 2293-2298 (1993)
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/clone_lib="mouse lung cDNA"
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/db_xref="GI:2809069"
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/chromosome="5"
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/product="flt-1"
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/clone="MD-9-11"
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FEATURES

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2145 TCGGGCACCTATGCGTGCAGAGCCAGAACATACACAGGGGAAGACATCCTTGGAAG, 2204
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BMRK2 gene: receptor kinase.
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/gene-"EmRK2"
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AVKMLKEGATASEYKALMTELKILITHIGHHLNVVNLLGAGTKOGGPLMVIVEYCKYGN
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/translation="MySCWDIAVLPYALLGCLLITGYGSGSKLKVPELSILKGTOHYMO
/translation="MySCWDIAVLPYALLGCLLITGYGSGSKLKVPELSILKGTOHYMOALPYALLGCLLITGYGSBTILTGYGGSTILTGYANH
IGLYCRYLDISISKKKAESSIYIFYSDAGSPFIEMHTDIPKLVHMIESGQLIICRY
ISPNYIVILKKFPFDILTPDGORITWDSRRGFIIANATYREIGLINCEAVNGHLYQIN
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IRQRIDRSHSHNNVFHSVLKINNVESRDKGLYTCRVKSGSSFQSFNTSVHVYEKGFIS
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Choi.K.: Wall, C., Hanratty, R. and Keller, G.
Tioolation of a gene encoding a novel receptor tyrosine kinase from differentiated embryonic stem cells
Oncogene 9 (4), 1261-1266 (1994)
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/protein_id="CAA55311.1"
/db_xrefv"G1:510665"
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/cell_type="embryonic stem
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                                     241 TCAGGCACCTATGCGTGCAGAGGCCAGGAATGTATACACAGGGGAAGAAATCCTCCAGAAG 300
                                                                                      2193 ACAGAAGTICTCGTIAGAGATICGGAAGCGCCACACCTGGTICAAAACCTCAGTGACTA 2252
                                                                                                                              301 AAAGAAAITACAAITGAGAAICAGGAAGCACCAIACCICCIGGGAAACCICAGIGAICAC 360
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1189 AGACGITICAAICAGAGGCAAGAGGCACCAGCTCIGCIGCGGGGGGGCTCAIGGAICAGAG 2248
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                                       2129 AGGCACCIAIACCIGCCGAGCAAGGAACATATICACGGGGAAAGAAGIGCTICAAAAGAA 2188
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                                                                                                                                                                                                                                                      303 AGAAATTACAATCAGAGGATCAGGAAGCACCATACCTCCTGCGAAACCTCAGTGATCACAC 352
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             CACTAAGGAGCACTCCATCACTCTTAATCTTACCATCATGATGTTTCCCTGCAAGATTC 242
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Submitted (11-2001) Masabumi Shibuya, University of Tokyo.
Submitted cf Medical Science, 4.6-1 Shirokane-dai. Minato-ku, Tokyo.
108-8639, Japan (E-mail:Shibuya@ims.u-tokyo.ac.jp.
Tel:81-3-5449-5550. Fax:81-3-5449-5425)
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GVSRSKESGLIGIIKPRSFCSFSCDQLSESKRRITGNIVLEKMKACHSPPDYSSVV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /product="vascular endothelial growth fartor receptor-1"
                                                                                     Yamaguchi, S., Iwata, R. and Shibuya, M. Soluble Fit-1 (soluble VECFR-1), a potent natural antiangiogenic molecule in mammals, is phylogenetically conserved in arians Biochem. Blophys. Res. Commun. 291 (3), 554-559 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1967 GAATCIGGIAIIGICCTGIICAGCCAACAAAIICAIGIACAAAGACAIIICEIGGAIIITE 2926
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Archosauria: Aves: Neognathae; Galliformes; Phasianidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 39,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /iote="fit-1
fms-like tyrosine kinase-1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /tissue_lib-"whole embryo"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Gallus gallus"
/db_xref="taxon:9031"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /protein_id="BAB84690.1"
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                                Phasianinae; Gallus.
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Best Local Similarity
                                                                                                                                                                                                                                                                      Shibuya, M.
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The transcriptional map of the common eliminated region 1 (332ER1) in 3p21.3
                                                                                                                                                                                                                                                                                                                                                                 On Apr 5, 2001 this sequence version replaced gi:13545633. The sequence is a consensus sequence of clone RP4-787c23 (1-140400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                28448-42160 bp Contig 5: 42261-55059 bp Contig 6: 55160-61578 bp
                            Kiss, H., Yang, Y., Kiss, C., Andersson, K., Klein, G., Imreh, S. and
Dumanski, J.p.
                                                                                                                                                                                                                                                         Direct Submission
Submitted (Ol-APR-2001) Kiss H., Microbiology and Tumorbiology
Center (MIC), Karolinska Institute, Box 280, Stockholm, S-7177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   **NOTE: This is a "working draft' sequence. It currently consists of 26 contigs. Gaps between the contigs are represented as runs of N. The order of the pieces is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have provided by the submittor.

**Ihis sequence will be replaced by the full be replaced by the full be replaced by the submittor.

**Ihis sequence will be preserved.

**Ihis sequence will be preserved.

**Ihis 21881: contig of 11731 bp in length 11832 1881: gap of 100 bp.

**Independent the submittor of 11731 bp in length 11832 1881: contig of 14387 hr. -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1-11731 bp Contig 2: 11832-26218 bp Contig 3: 26319-28347 kp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     and clone RP5-188g11 (partially, 1-108303 bp). The sequencing
                                                                                                                                                                                                                                                                                                                                                                                                                                                cione RF6-32g23 (31212-220965 bp), clone RF6-146e1 (partially,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        in order and the gaps between them are represented by 100 Ks.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               133628-189031 bp Contig 18: 189152-189476 bp Contig 19: 189577-191375 bp Contig 19: Contig 20: 191476-201473 bp Contig 21: 201574-202307 bp
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131848-132316 bp
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                                                                                                                              Hum. Genet. 10 (1), 52-61 (2002)
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Contig 10: 118828-121834 bp
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                                                                                                                                                                                                               (bases 1 to 220955)
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42351 55059:
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                                                                                                                                 Eur. J. H
21905202
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                                                                                                                                                                                      11896456
                                                                                                                                                                                                                                         Kiss, H.
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Homo sapiens chromosome 3 clone RP6-32923 map 3p21.3, ***
SEQUENCING IN PROGRESS ***, 26 ordered pieces.
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Eukaryota: Metazoa: Chordata: Craniata: Vertebrata: Euteleostomi;
Mammalia: Eutheria: Primates: Catarrhini: Hominidae: Homo.
                                                                                                                                                                                                                                                                                                                                                                                                1434 TCITITAICTGAGAACAACGTGGTGAAGATITGTGATTTTGGCCTTGCCGGGATAITTA 1493
                                                                                                                                                                                                                                                                                                                       1329 CCITITATCIGAGAAGAIGTAGIGAAGAICTGIGATIIIGGCCTGGCAAGAGAIAITTA 3388
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GCTGIGGGAAATCTICICCTTAGGIGGGTCTCCATACCCAGGAGTACAAATGGAIGAGA 1673
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AJ312688.2 GI:13559235
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Romo. 1 (bases 1 to 197279) (Saul.R.K., Olson,M.V., Zhou,Y., James,R.A., Rouse,G., Wu,Z., Saenphimmachak,C., Phelps,K.A., Buckley,D., Kibukawa,M., Raymond,C. and Haugen,E.D.
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Submitted (20-JUN-2002) Genome Center, University of Washington,
BOX 352145, Seattle, WA 98195, USA
On Jun 20, 2002 this sequence version replaced gi:1748851.
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                                                                                                                                                                                                                                                                                                           IGAGIACTCTACTCCIGAAATCTATCAGATCAIGCIGGACTGCTGGCACAGAGACCCAAA 1775
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AC104439.2 GI:21490240
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                                                                GIGGICTIACGGAGIAIIGCIGIGGGAAAICTICICCTTAGGIGGGICICCATACCCAGG
                                                                                             1776 AGAAAGGCCAAGATIIGCAGAACTIGIGGAAAAACTAGGTGATIIGCIICAAGCAAAIGI
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Kaul,R.K., Olson,M.V., Raymond,C. and Haugen,E.D.
Direct Submission
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Saenphimmachak,C., Phelps,K.A., Buckley,D.,
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Center: University of Washington Const.	Center Code: UNGC Web Site: http://www.nenomo.mais.com	Contact: uwgchtgs@u.washington.edu Drafting Cepter: Wick	Center project journation	Center clone name: RP11-793E15 (bc0564)	Sequencing vector unknown; 52% of reads	Chemistry: Dye-terminator E1: 94% of reads Chemistry: Dye-terminator E1: 94% of reads Chemistry: Dve-terminator nichten e2: 100%	Assembly program: Phrap, version 0.990319 Consenses mallet v 10716 because	Consensus quality: 197255 bases at least 040	Insert size: 1972/9; sun-of-contigs Onality coversor of 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2	Overlanding Sequences	5': R21-91E8 (UMGC: bc0216) AC026349 3': CID-2563A18 (UMGC: bc023A)	Sequence One lite Accessor.	This entry has been annotated with sequence quality estimates computed by the phran accembir never and	All manually edited bases have the reduced that I sero. Quality levels above 40 are expected to have local than	TESS CHAI	GenBank flat file format but are available as part of this entry's ASN.I file.	This sequence was finished as follows unless otherwise.	all regions were either double-stranded or sequenced with an alternate chemistry or covered by high annieths and sequenced with an alternate chemistry or covered by high annieths and sequenced with an alternate chemistry or covered by high annieths and alternate chemistry or covered by the cov	quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and reneats.	covered by at least one plasmid subclone or more than one Hi3 subclone; and the assembly was confirmed by restriction.	Sequence Validation:	This sequence has been validated by Multiple Complete Digest fingerprinting. Comparison of the experimentally documentals.	fragments with sequence-predicted international period digest The electronically-digested sequence consists of both small new	vector, in order to accurately represent the entire circular BAC. Small fragments below a variable cutoff (annowimstel) notice in the control of the control	are not resolved in the fingerprint and here.	between the experimental and predicted values. Uniquely ordered fragments are separated by dashed lines.	Hindiii Bglii EcoRI	SeqDerMap FngrPrnt SeqDerMap FngrPrnt SeqDerMap FngrPrnt		2687 2517 8949 8586 8595 8551	6382 6410 2057 2160 6 <800	512 <800 7846 7940 2742 2803	449 <800 3734 3895 5324	2602 2763 1334 1301 1493 1478	2590 2617 2287 2309 823 835	8313 8291 1914 1918 1962 2002	

OY 1715 TGAGTACTCTACTCCTGAAATCTATCAGATCATGCTGGACTGCTGGCACAGAGACCCAAA 1775 Db 68048 TGAGTACTCTGCTGAAATCTATCAGATCATGCTGGACTGCTGGCACAAAGCCCAAA 1775 Db 68048 TGAGTACTCCTGAAAATCTATCAGATCATGCTGCACACAAAGCCCAAA 67989 OY 1776 AGAAAGGCCAAGATTGCAGAACTTGTGGAAAAAATTGCTTCAAGCACAAATGT 1835 HIHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHH	5076 57688 SULT 11 481480 FINITION EESSION EES	Ouery Match Best Local Similarity 65.3%; Pred, No. 3.8e-197; Matches 1077; Conservative 0; Mismatches 562; Indels 6; Gaps 2; Matches 1077; Conservative 0; Mismatches 562; Indels 6; Gaps 2; Oy 218 TCATGANICITICCTICCANGAGATICAGGAGGCCAGGAGGCAGGAGGAGGAGGAGGAGGAGGAGG
6998 7317 431 <80C	Query Match 45.4%; Score 953.2; DB 9; Length 197279; Best Local Similarity 94.5%; Pred. No. 5.4e-267; Aatches 988; Conservative 0; Mismatches 58; Did Gest Qy 1056 Acgccrcrcaractionedraticinanary Acgccrcrcaractionedraticinanary Did Gest Did	0y 1416 CCTGGCAGCGAGAAACAIICIIIAICIGAGAACAAGGIGGIGAAGAIITGIGAIIIIGG 1475 bb 68348 CCTGGCAGGAAACAIICIITAACIGAGAAAGGIGGIGAAGAIITGIGAIIIIGG 68269 0y 1476 CCTGGCCGGGAAATIIATAAGAAACCCGAAIAAGGAGAAACGAGATACCGACTICC 1535 151

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458 AAGAGCCIGGAAIIAIIIIASGACCAGGAAGCAGCACCCIGIIIAIIGAAAGAGICACAG 517
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                                                                                                                                          CIGAGIACTCIACICCIGAAATCIATCAGAICCIGGACIGCIGGCACAGAGACCCAA 1774
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Patent: US 5204011-A 1 20-MAR-2001;
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34.0%; Score 713.8; DB 6;
Best Local Similarity 65.5%; Pred. No. 3.8e-197;
Matches 1077; Conservative 0; Mismatches 562:
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(Kendall, R. L. Mao, X., Thomas, K.A. an +Human receptor tyrosine kinase, KDR patent: US 6359115-A 1 19-MAR-2002;
                                                                                                                                                                                                                         Sequence 1 from patent US 6359115.
AR201382
AR201382.1 GI:20252270
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                                                                                                                                                            Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Rutele
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Method for inhibiting the expression of a target gene
Patent: WO 02055593-A 97 18-JUL-2002;
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Pred. No. 3.8e-197;
0; Mismatches 562;
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Sequence 97 from Patent WO02055693.
AX481483
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/db_xref="taxon:9606"
894 c 1025 q 98
1935 IACAACAGGAIGGIAAAGACIACAI 1859
              3503 CICAGCAGGAIGGCAAAGACTACAI 3527
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                                                       875 ITCAAGCAICAGCAITIGGCAIIAAGAAAICACCIACGIGCCGGACIGIGGCTGIGAAAA
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AF053558 4071 hp mRNA linear PRI 16-MAY-1998 Homo sapiens vascular endothelial growth factor receptor 2 (KDR)
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VGYRIYDVVLSPSHGIELSVGEKLVLNCIARTELNVGIDFNWEYPSSRHGIRKLVNRD
LKTQSGSEMKKFLSYLIIDGVTRSDQGLYTCAASSGLMTKKNSIFVRVHEKPFVAFGS
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GKNKIVSTLVIQAANVSALYKCEAVNKVGRGERVISTHYTRGPETILQPPMQPTEQES
VSLRCIADRSTFENLTWYKLGPQPLPIHVGELPTPVCKNLDTLWKLNATMFSNSTNDI
LIMELKNASLQDQGDYVCLAQDRKTKRRHCVVRQLIVLERVAPTITGNLENQTISIGE
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VLASEELKILEDRIKLSPSFGGWPSKSRESVASEGSNQTSGYGSGYHSDDIDIIVYS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /translation-"MESKVLLAVALWLCVETRAASVGLPSVSLDLPRLSIQKDILTIR
ANTILQITCRGQRDLDWLMPNNQSGSBQRVEVTECSDGLFCKTLTIPKV1GNDTGAYK
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IGNYIVILINPISKEKOSHVVSLVVYVPPPQIGEKSLISPVDSYQYGTIQTLICTVYRJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CFYREIDLASVIYVYVQDYRSPFIASVSDQHGVVYIIENKNKTVVIPCLGSISNLNVS
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SVLGCARVEAFFIIESAQEKINLEIIILVGTAVIAMFFWLLLVIILRIVKRANGGELK
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DKIAICRIVAVKMLKEGATHSEHRALMSELKILIHIGHHLNVVNLLGACIKPGGPLMV
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ARNILLSEKNVVKICDFGLARDIYKDPDYVRKGDARLPLKWMAPETIFDRVYT10SDV
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae: Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (05-MAY-1998) Adirondack Biomedical Research Institute.
10 Old Barn Rd., Lake Placid, NY 12946, USA
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /product="vascular endothelial growth factor receptor/protein_id="AAC16450.1"
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Yu.Y., Whitney, R.G. and Sato, J.D.
Codding region for human VEGF receptor KDR (VEGFR-2)
Unpublished
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Pred. No. 3.8e-197;
0; Mismatches 562;
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/cell_type="endothellum"
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Copyright (c) 1993 - 2002 Compugen Ltd.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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/*tag= d /standard_name= "Single nucleotide polymorphism (SNP).

/*tag= c replace (696, C)

variation

EP1130123-A2.

/*tag=: a 580..664 /*tag- b 665..1256

> exon, intron

Cocation/Qualifiers

intron

Homo sapiens

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AA2512 AAV744 ABQ881 ABL075 ABL272 ABL272 ABL042	AAK649 AAK649 AAK716 AAT811 ABK360 AAI952 AAD0834	ABK1497 AAS463.4 AAF6324 ABK8524 ABK8556 AAI9676 AAI9676	AA205332 AA206815 ABL34292 ABL34292 AA446510 AAC17824 AAKS1410 AAKS145 AAR31045 AAR36555 AAS14506	ALIGNMENTS BP. T #5. T haemostatic; 9e: arthitis; endometis; voluments; vol	acor, single nucl
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This isolated polynucleotide codes for the Staphylicoccus aureus KNA-uspendent amidotransferase C (ketC) protein (see ANM61464). It was contained from a library of clones of chromosomal DNA of S. aureus in E. coll. S. aureus WOH 29 strain containing the coll. S. aureus WOH 29 strain containing the full length rail gene is deposited as NOTME 1071. The inventor provides vectors compision the isolated polynucleotide, lost certain professions and antagonists. The rate polypeptide is used to treat an individual with the read of rate and the intagonist is used to treat an individual with the read of inhibit rate. Dispeptide is used to treat an individual with the read of inhibit rate. Dispeptide is used to treat an individual with the reducting rate. The comprises determining a mucleic acid sequence encoding rate and of a dispense related to expression or aciditie, or analysing for the presence or amount of rate in a sample. The fact or a fraguent or variation are vector expressing it is used to induce an immunication response, adequate to produce an anticoup and/or a frequence response the vector is delivered in vivo) and/or a frequence response the vector is delivered in vivo) and/or a frequence response the vector is delivered in vivo) and/or a frequence response the vector is delivered in vivo) and/or a frequence response the vector is delivered in vivo) and/or a frequence response the vector is delivered in vivo) for the active agence engineering the active agence and and add address in the delivered in vivo) for read intections of the upper response and and add address in a delivered in vivo) for read intections of the upper response and and address in a delivered disorders describe engagement and and address in the delivered and address and address and delivered disorders delivered disorders (e.g. engagement and disorders).
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                                                                        a
"may be amended by X-(R1)n- group, where X
Is H. R1 is any nucleic acid residue, and
is 1-1000"
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                                                                                                                                                                                                                                                                                              may be amended by (R1)n-Y- group, where is H or a metal, R2 is any nucleic acid residue, and n is 1-1000^\mu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               disorders (e.g. secretory diarrhoea, splenic absoess and retroperitoneal absoess), CNS disorders (e.g. cerebral absoess), eye disorders (e.g. blepharitis, conjunctivitis, keratitis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            31.7%; Score 32;
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (SMIK ) SMITHKLINE BEECHAM CORP. (SMIK ) SMITHKLINE BEECHAM PLC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 4; Page 6; 32pp; English.
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9705-0044365.
9705-0044366.
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                                                                        /*tag=
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI: 1998-416607/36.
P-PSGB; AAW61464.
                                                                                                                                                                                                                          misc_difference 300
                            misc_ulfference
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             38 AIGCOITTICCIGICTIGATAATTCITTCICTICATIAGATAIGTAAAIGCTTICA 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Isolated polynucleotide encoding polypeptide expressed Ly Staphylococcus aureus - used e.g. to treat infections of upper and lower respiratory tract, cardiac system and gastrointestinal tract
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Staphylococous aureus RNA-dependent amidotransierase U (ratC) ye…e.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              blepharitis; conjunctivitis; keratitis; endophthalmitis;
cellulitis; darcryocystitis; epididymitis; intrarenal access;
perinephric abscess; toxic shock syndrome; impetigo; folliculitis;
cutaneous abscess; myositis; septic arthritis; osteomyelitis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ratt: RNA-dependent amidotransferase C; antibiotic; antibacterial;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This isolated polynucleotide codes for the Staphylococcus aureus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RNA-dependent amidotransferase C (RatC) protein (see AAW51459).
Novel ratB polypeptides of the invention (see AAW61457) ...ay
interact with ratC and/or ratA (see AAW61470) polypeptides to
form ratB:ratC and ratB:ratA heterodimers or ratB:ratA:ratC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          interornimers. Such heterodimers and heterornimers are useful in methods of the invention, particularly vaccine and using SCreening methods, e.g. for assays of ratB antagonists useful as antibacterial agents.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         empyaema; lung abscess; infective endocaratis; diarribea; splenic abscess; retroperitoneal abscess; cerebral abscess;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        31.7%; Score 32; DB 19; Length 355; 68.8%; Pred. No. 3.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         otitis media, tracheitis; acute epiglottitis; thyrolditis;
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0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure; Page 16; 34pp; English.
                                                                                                                                                                                                                                                                                                                                                                                               (SMIK ) SMITHKLINE BEECHAM CORP. (SMIK ) SMITHKLINE BEECHAM PLC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Lewis CJ;
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ID AAV45098 standard; DNA; 300 BP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Lawlor EJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WFI; 1998-416008/36.
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                                                                                                                                 04-FEB-1998;
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28-APR-1997;
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syndrome), skin disorders (e.g. imperigo, folicalitis, clearedus abscesses, cellalitis, wound infection and bacterial myositis) and bone and joint disorders (e.g. septic arthritis and usternayeilitis), to assay genetic variation and to screen for antibacterial agents.
                                                                                                                                                                                                                                                                  Sequence 300 BA: 121 A: 48 C: 61 G: 70 T; 0 other;
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DB 19;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Staplylococcus aureus DNA for cellular proliferation protein +1368.
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byce: The sequence data for this parent did not form part
of the printed specification, but was obtained in electronic
locate directly from WIPO at.
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ive 0; Mismatches 20; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Antisense, ds, prokaryotic cellular proliferation gene, antibiotic, antibacterial, drug design.
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Xu HH;
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2000US-207727P.
2000US-242578P.
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2001US-269308P.
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Matches 44; Conservat
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5ê AGTT 101
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27-1:4-7-2000;
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Yamamoto RE,
                                                   13-FEB-2002
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The invertion relates to antisense inhibitors of genes essentia, to prokaryotic cellular proliferation, their use in identifying the genes. Their use in the discovery of novel artiblotics, the essential genes translates and the encourage from the prokaryotes used are Escherichia coli, Staphylococcus aureus, Salmodella upphi, Klebsiella preumoniae, Pseudomonas acusinosa and Enterococcus fecalis. The invention is also useful for the identification of potential new rangets for antiblotic development. The antisense nucleic acids can also be used to descript proteins used in proliferation, to express these proteins, and to obtain antibloties capable of binding to the expressed proteins. The proteins can be used to screen compounds in rational drug discovery programmes. The antisense nucleic acid sequence is also useful to screen for homologous nucleic acids which are required for poliferation in
38 AIGCUITTICCIGICTEGAIAATTOTTICTICTICATTRGATATGTAAATGCTTICA 97
                                                 104 ACCULLICIAN FOR THE FILL T
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Staphylobocous auréus DNA for cellular proliferation protein #1442.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Antisense; ds. prekaryotic celidiar prolliferation generantici. Julio; antibacterial; drug design.
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AASSSIBO/c
ID AASSSIV standard; DNA; 303 BP.
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2000US-242578P.
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200108-269308P.
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Yaman.co RI, Xu HH:
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2 - DEC - 2000;
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This sequence represents one of 5191 Staphylococcus aureus DNA sequences of the invention. The DNA sequences are recorded on a computer readable and thus in preferably selected from a floppy or hard disx, random access memory (RAM) read-only memory (ROM) or CD-ROM. Homology searches using the S.aureus DNA sequences allows putative functions to be assigned so that protein-encoding or regulatory regions of commercial, therapeutic or indiantial importance can be obtained. Specifically, sequences which are likely to encode antigens have been identified and these polypeptides can be used in a vaccine composition against S.aureus infection. The polypeptides can also be used in a kit for the immunodatection of solutions as a sample. S.aureus is implicated in numerous human diseases, including ceilulitis, eyelld infections, food poisoning, osteomyelitis, skin and surgical wound infections, scalded skin syndrome, toxic shock syndrome, etc. Organisms transformed with the DNA sequences can be used to the polypeptides. The new DNA sequences can be used to the polypeptides. The new DNA sequences can be used to the polypeptides. The new DNA sequences can be used to the polypeptides. The new DNA sequences can be used to the polypeptides. The new DNA sequences can be used to the polypeptides.
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                      9 "these bases represent a line of missing text in the sequence listing in the specification. They are included to maintain the nucleotide numbering given in the specification for this DNA sequence"
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Pred. No. 6.8;
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68.8%;
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      misc_feature
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Rosen CA;
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the sequence listing in the specification. They
are included to maintain the nucleotide numbering
given in the specification for this DNA sequence"
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the sequence listing in the specification. Itsy
are included to maintain the nucleotide numbering
given in the specification for this DNA sequence"
conjunctivitis, osteomyelitis, skin infections and toxic shock syndrome. The present sequence is also useful for detecting Staphylococcal infections in biological samples.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Computer readable medium; vaccine; S.aureus infection; immunodetection; cellulitis; eyelid infection; food poisoning; osteomyelitis; therapy; skin infection; surgical wound infection; scalded skin syndrome;
                                                                                                                                                                                                                        Gaps
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                                                                                                                                                              0;
                                                                                                                31.7%; Score 32; DB 21; Length 3400; 68.8%; Pred. No. 5.1;
                                                                               Sequence 3400 BP; 1256 A; 510 C; 648 G; 986 T; 0 other;
                                                                                                                                                            0; Mismatches
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/note=
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                           Venter JC, Adams M,
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                                                                                                                                                                                                                                                                                             The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention is useful in developmental blology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABB1737-ABB12073).

The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
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                                                                                                                                                                                                                 New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signalling and cell-cell
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Pred. No. 18;
0; Mismatches 28; Indels 0;
                                                                                                                                                                                                                                                                   Claim 1; SEQ ID NO 33307; 21pp + Sequence Listing; English.
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                                                                                                                                                                Li PWD, Myers EW;
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62.7%;
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11-JUL-2000; 2000US-0614150.
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11-JUL-2000; 2000US-0614150.
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                                                                                                                                                              Venter JC, Adams M,
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capable of dececting 1000 or more genes from brosophila. The invention is useful in developmental blology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL16176-ABL30511), expressed DNA sequence (ABL16176-ABL30511), in expressed DNA sequence (ABS7737-ABS7737-ABS7737-ABS7737-ABS7737-ABS7737-ABS7737-ABS7737-ABS7737-ABS7737-ABS7737-ABS7737-ABS7737-ABS7737-ABS7737-ABS7737-ABS7737-ABS7737-ABS7737-ABS7737-ABS7737-ABS7737-ABS7737-ABS7737-ABS7737-ABS7737-ABS7737-ABS7737-ABS7737-ABS7737-ABS7737-ABS7737-ABS7737-ABS7737-ABS7737-ABS7737-ABS7737-ABS7737-ABS7737-ABS7737-ABS7737-ABS7737-ABS7737-ABS7737-ABS7737-ABS7737-ABS7737-ABS7737-ABS7737-ABS7737-ABS7737-ABS7737-ABS7737-ABS7737-ABS7737-ABS7737-ABS7737-ABS7737-ABS7737-ABS7737-ABS7737-ABS7737-ABS7737-ABS7737-ABS7737-ABS7737-ABS7737-ABS7737-ABS7737-ABS7737-ABS7737-ABS7737-ABS7737-ABS7737-ABS7737-ABS7737-ABS7737-ABS7737-ABS7737-ABS7737-ABS7737-ABS7737-ABS7737-ABS7737-ABS7737-ABS7737-ABS7737-ABS7737-ABS7737-ABS7737-ABS7737-ABS7737-ABS7737-ABS7737-ABS7737-ABS7737-ABS7737-ABS7737-ABS7737-ABS7737-ABS7737-ABS7737-ABS7737-ABS7737-ABS7737-ABS7737-ABS7737-ABS7737-ABS7737-ABS7737-ABS7737-ABS7737-ABS7737-ABS7737-ABS7737-ABS7737-ABS7737-ABS7737-ABS7737-ABS7737-ABS7737-ABS7737-ABS7737-ABS7737-ABS7737-ABS7737-ABS7737-ABS7737-ABS7737-ABS7737-ABS7737-ABS7737-ABS7737-ABS7737-ABS7737-ABS7737-ABS7737-ABS7737-ABS7737-ABS7737-ABS7737-ABS7737-ABS7737-ABS7737-ABS7737-ABS7737-ABS7737-ABS7737-ABS7737-ABS7737-ABS7737-ABS7737-ABS7737-ABS7737-ABS7737-ABS7737-ABS7737-ABS7737-ABS7737-ABS7737-ABS7737-ABS7737-ABS7737-ABS7737-ABS7737-ABS7737-ABS7737-ABS7737-ABS7737-ABS7737-ABS7737-ABS7737-ABS7737-ABS7737-ABS7737-ABS7737-ABS7737-ABS7737-ABS7737-ABS7737-ABS7737-ABS7737-ABS7737-ABS7737-ABS7737-ABS7737-ABS7737-ABS7737-ABS7737-ABS7737-ABS7737-ABS7737-ABS7737-ABS7737-ABS7737-ABS7737-ABS7737-ABS7737-ABS7737-ABS773
                                                                                                                                                                                                                                                                                                                                                                                                                         New isolated nucleic acid detection reagent for detecting 1000 or more genes from Droscohila and for elucidating cell signalling and cell-cell
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ine invention relates to an isolated nucleic acid detection reagent
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AC19379 Rettus no
AC081068 Homo sapi
AC128656 Rettus no
AC126108 Rettus no
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AC13537 Mus muscu
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Human DNA sequence from clone RP11-502P18 cr chromosome 13,
completes sequence.
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Mammalia; Lutheria; Primates; Catarrhini; Huminidae; Homo.
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sects greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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AUTHORS
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Direct Submission

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Brown, A., Castle, A., Colaugelo, M., Collins, S., Collymore, A., Cooke, P., Dearellano, K., Dewar, K., Domino, M., Donelan, L., Doyle, M., Errest, C., Furke, R., Gage, D., Galagan, J., Gardyan, S., Grant, G., Hayos, E., Hardyan, S., Grant, G., Hayos, E., Hardyan, S., Grant, G., Hayos, E., Hardyan, J., Cardyan, S., Grant, G., Hayos, E., Hardyan, S., Grant, C., Kann, L., Karatas, A., Klein, J., Howland, J.C., Johnson, R., Jones, C., Kann, L., Karatas, A., Klein, J., Morrow, J., Naylor, J., Norman, K., Modoughd, P., Marquis, N., Morrow, J., Naylor, J., Norman, C. H., O'Confor, T., O'Donnell, P., Belterson, K., Pollara, V., Kiley, R., Roy, A., Sautos, R., Severy, P., Stange-Inoman, N., Stojanovic, N., Suframanian, A., Talanas, J., Tesfaye, S., Tirrell, A., Vassillev, H., Vo, A., Kheeler, J., Wu, X., Myman, D., Ye, W.J., Zinmer, A., and Zody, M., Kheeler, J., Wu, X., Kiley, M., Kand, J., Zinmer, A., and Zody, M., Kheeler, J., Wu, X., Kheeler, J
                                                                                                                                                                                                                                                                                                                                                                                                            Direct Submission
Submitted (24-NOV-1999) Whitehead Institute/MII Center for Genome Submitted (24-NOV-1999) Whitehead Institute/MII Center for Genome Research, 320 Charles Street, Campridge, MR. 02111, USA On Apr 16, 2000 this sequence version replaced gi:6970658.

All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.wasfington.edu/RM/RupeatMasker.html
http://ftp.genome.wasfington.edu/RM/RupeatMasker.html
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NOTE: This record contains 246 individual sequencing reads that have not been assentied into contligs. Runs of N are used to separate the reads and the order in which they appear is completely
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1332 3431: contig of 774 bp in length
3332 3431: gap of 100 bp
3432 4213: contig of 782 bp in length
4214 4313: gap of 100 bp
1314 5079: contin of 782 bp in length
1314 5079: contin of 782 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9485: gap of 100 bp
10285: contig of 773 bp in length,
10358: gap of 100 bp
11138: contig of 780 bp in length,
11238: gap of 100 bp
12014: contig of 776 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100 bp in length 100 bp 100 bp 100 bp 1701; gap of 100 bp 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      00 bp
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                728 827; gap of 100 hr in leagun
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9385: contig of 770 bp in length
9485: gap of 100 bp
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12876: contig of 762 bp in Leagua
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ool 100 bp contig of 781 bp in length
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749 bp in 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Web site: http://www-seq.wi.mit.edu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Center clone name: 27_H_10
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13758 13857; gap of
13858 14618; cont.
14619 14718; gap of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1702 2457. 2458 2557: gap of 2458 2557: gap of 2458
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6817: con
6917: gap of
7656: con
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8515: con
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2 (bases 1 to 224450)
Birren,B., Linton,L., Nusbaum,C., Lander,E., Ailen,N., Anderson.M
BaldWin,J., Barna,N., Beckerly, R., Boguslavkly,L., Boukhyalter,B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        76720 AIATGGIGCCTGTGGTCTCCTGACTCATTAGACTGGGTGCCTTITCCTGTCTTGATAA1 76661
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="MER3 repeat: matches 1. .193 of consensus"
46166. .46290
/note="LlNc5 repeat: matches 7756. .7525 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     , 1 ATATGGTGCCTGTGGTCCTGACTCATTAGAGCTGGATGCCTTTTCCTGTCTTGATAAT 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           39114, 39348
/note="MIR repeat: matches 4. .231 of consensus"
40010, 40203
/note="AluJo repeat: matches 86. .274 of consensus"
40286, 40581
                                                         32946. .33076
/Anote="FLAM.A repeat: matches 1. .133 of consensus"
33231. .33323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="MIR repeat: matches 118...222 of consensus"
334333. 33747
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           note="MERSA repeat: matches 1. .186 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="AluSp_repeat: matches 1. .297 of consensus" 41033. 41330 43730 7500 7599 of consensus" 43786. .43571
                                                                                                                                                                                                                                                                        35242. 35605
/note="THELB repeat: matches 1. 364 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                    .169 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    note="MER5B repeat: matches 1. .177 of consensus"
                                   .189 of consensus'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .241 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .189 of consensus*
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46598. .46767
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ACU16311 224450 bp DNA linear HTG 16
HOMO Sapiens clone RP11-27H10, LCW-PASS SEQUENCE SAMFLING
AC016311
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Birron, B., Linton, L., Nusbaum, C. and Lander, E. Gnoo, spiens, clone RP11-27H10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 164519;
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                                                                                                                                                                                                                                                                                                                                     35886. 36063
/note="89 copies 2 mer tt 57% conserved"
36786. 36959
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                                                                                                                                                                                                                                 /note="AluYb8 repeat: matches 1.
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                                'note="MER5A repeat: matches 4.
                                                                                                                                                                                                                                                                                                                                                                                                                    16786. .36959
/hote="MER20 repeat: matches 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         'note="MIR repeat: matches 131.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="MER5A repeat: matches 8.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 99.4; DB 9;
Pred, No. 4.5e-17;
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Cleveland, C.D., Cox, C., Coyle, M.D., Dathorne, S.R., David, R.D.

Davila, M.L., Davis, C., Davy-Carroll, L., Dederich, D.A.,

Delmapy, K.M., Delgado, O., Denna, H.D., Ding, Y., Dind, H.H.,

Douthwalte, K.J., Draper, H., Dugan-Rocha, S., Durchn, K.J.,

Falls T., Ferraguro, D., Flaga, N., Ford, J., Poster, P., Frantz, P.,

Falls T., Ferraguro, D., Flaga, N., Ford, J., Poster, P., Frantz, P.,

Gabisi, A., Gao, J., Garcia, A., Garrer, T., Garza, N., Gill, R.,

Harris, C., Harris, K., Hart, M., Havlak, P., Hale, S., Hamilton, K.,

Hernandez, O., Hodgson, A., Hogues, M., Bolloway, C., Hollins, B.,

Homsi, F., Howard, S., Huber, J., Hulk, S., Hume, J., Jackson, E.,

Jacobson, B., Via, Y., Johnson, R., Joluck, S., Joucah, J., Kovar, C.,

Kratovic, J., Kureshi, A., Landry, N., Leal, B., Lewis, L.C., Lewis, L.,

Lozdo, R.J., Lu, L., Lucker, R., Liu, M., Liu, W., Louseget, R.,

Manssey, B., Marhiney, B., Martin, R., Martindale, A., Martinez, E.,

Mansey, M., Mahua, P., Martin, R., Martindale, A., Martinez, E.,

Muner, G., Miner, Z., Mitchell, T., Wohabbat, K., Morgan, G.,

Nordon, N., Ovledo, R., Primus, E., Pull, L., Quiles, M., Berris, S.,

Rives, M., Rodjas, A., Roluokan, I., Rolie, M., Mells, S., Sarery, S.,

Scherer, S., Soalek, R., Roluokan, I., Rolle, M., Mells, S., Sarery, S.,

Soderyen, E., Sonaike, T., Sparks, A., Stanley, H., Stone, H.,

Sutton, A., Svatek, A., Tabor, P., Tamerisa, R., Tanerisa, K.,

Wang, S., Ward-Moore, S., Warren, R., Washington, C., Watlingson, B.,

Wall, S., Ward-Moore, S., Warren, R., Washington, C., Watlingson, B.,

Wall, S., Wall, Way, F., Zhou, J., Zorrilla, S., Wallson, D.,

Wall, S., Wall, Way, F., Sou, J., Zorrilla, S., Wallson, D.,

Wall, S., Wall, S., Rou, J., Zorrilla, S., Wallson, D.,

Wall, S., Wall, W.Y., Wu, Y.F., Zorrilla, S., Wallson, D.,

Wall, S., Wall, Wall, R., Rou, J., Zorrilla, S., Walley, R., Rou, J., Zorrilla, S., Walley, R.,

Wall, S., Wall, W.Y., Wu, Y.F., Zorrilla, S., Walley, R., Wall, M., Walley, R.,

Wall, Wall, S., Walley, R., Walley, R., Walley, R., Walley
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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Assembly program: Phrap; version 0.990329
Consensus quality: 55655 bases at least Q40
Consensus quality: 59929 bases at least Q50
Consensus quality: 62415 bases at least Q20
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contig of 1008 bp in length
gap of unknown length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: hgsc-help@bcm.tmc.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Center clone name: CH230-69N22
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Worley, K.C.
Direct Submission
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AUTHORS THILE JOURNAL

COMMENT

TITLE JOURNAL REFERENCE

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Submitted (14-701-2002) Department of Genetics, Washington University, 1414 Forest Park Avenue, St. Louis, Missouri 63108, USA. On Jul 4, 2002 this sequence Version replaced gi:20340525.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mapping information for this clone was provided by Dr. John D. Wefburson, Department of Genetics, Washington University, St. Louis Mo. P. additional information about the map position of this sequence, see http://genome.wustl.edu/ssc
                                               Direct Submission
Suchitica (04-MAR-2002) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 83108, USA
                                                                                                                                                                                                                                              Louis,
                                                                                                                                                                                                                                                                                                                                                                                         Louis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This sequence was finished as follows unless cinerwise noted: all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (1.e., phred quality >-30); an attempt was made to resolve all sequencing problems such as compressions and repeats, all regions were covered by sequence from more than one subclone; and the assembly was confirmed by
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The APCI-11 human BAC library was made from the blood of one male doctor, as described by Oscepawa.K., Wood,P.Y., Zhao,B., Frengen,E. Tatuco,M., Catanese,J.J. and de Jony,P.J. (1996) An improved appriach for construction of bacterial artificial chromosome libraries. Genomics 51:1-8. The clone may be obtained either from Research Genetics, Inc. (http://www.resyen.com) or Pleter de Jong VECIOR: IPBACe3.6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NOTICE: This sequence may not represent the entire insert of this close. It may be shorter because we only sequence overlapping close sections once, or longer because we provide a small overlap between neighboring data submissions.
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The clone sequenced to the right is RFI1-62F16, 2000 bp overlap.
Actual start of this clone is at base position I of RFI1-373H2;
actual end is at base position 63477 of RFI1-62F16.
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                                                                                                                                                                                                                                                                                                                                                         mitted (04-JUL-2002) Genome Sequencing Center, Washington easily School of Medicine, 4444 Forest Park Parkway, St.
                                                                                                                                                                                            Direct Submission
Submission Submission
Submission (30-APR-2002) Genome Sequencing Center, Washington
University Scrool of Medicine, 4444 Forest Fark Parkway, St.
MO 63108, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Center: Washington University Genome Sequencing Center
Center code: WUGSC
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/db_xref="taxon:9606"
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3 (bases 1 to 96559)
Waterston, R.H.
                                                                                                                                      4 (bases:1 to 96559)
Waterston, R.H.
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Waterston, R.H.
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DD :62057 CIGIGGICACCATTTICATGATAACTGAGGCTIACCGICTITAICIIIIIIIII 61998
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Homo sapiens BAC clone RP11-373H2 from 2, complete sequence.
AC113610
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 36.6; DB 2; Length 170443; Pred. No. 3.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .;
0
                                                                                                                                                                                                                                              95570 95655.gap of 100 bp 95570 95655.gap of 100 bp 95670 131654; contig of 35985 bp in length 131655 131754; gap of 100 bp 131755 170443; contig of 38685 bp in length.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       704 others
                                                                                                        16556 17055; gap of 100 bp in length.
17056 28121: contig of 11066 bp in length.
28122 28221: gap of 100 bp in length.
2822 60294: contig of 32073 bp in length.
60295 60394: gap of 100 bp in length.
60395 60394: gap of 100 bp in length.
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Abbott,S., Haakenson,W. and Creason,K.
The sequence of Homo sapiens EAC clone RPII-373H2
Upublished (2001)
                                                                                                                                                                                                           ap of 100 bp contig of 35175 bp in length
                      of 100 bp
contig of 6564 bp in leagth
                                                                   of 100 bp
contig of 9238 bp in length
contig of 953 bp in length.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               /clone_lib="RPCI-24 Male Mouse BAC"
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Toward a complete human genome sequence
Genome Res. 8 (11), 1097-1108 (1998)
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131755. .170443
/note="assembly_fragment"
a 32488 c 32968 g 45630 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   17056. .28121
/note="assembly_fragment"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                'note="assembly_fragment"
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/note="assembly_fragment"
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'note="assembly_fragment"
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/note="assembly_fragment"
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                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Mus musculus"
/db_xref="taxon:10056"
/clone="RP24-472H5"
         3: gap of
7617: con*
                                                                   7: gap of
16955: con
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Best Local Similarity
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AC113610/c
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AUTHORS
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Parabola, J. Bandanunge, K. Blankenburg, K. Bendania, J. Berdania, J. Bendon, J. Bindenburg, K. Bondania, J. Bendon, J. Bindenburg, K. Bondania, J. Bendon, J. Bindenburg, K. Brown, M. Bryant, N. Buok, J. Bonde, S. Brieda, M. Brown, E., Brown, M. Bryant, N. P. Bouck, J. Burcher, M. Cavazos, S.R., Chacko, J. Chavez, D. Chen, C. Chowdry, I., Christopoulos, C. Chen, R. Chen, Z., Chowdry, I., Christopoulos, C. Cavida, M. Dandense, S.R., David, R., Devlan, M. L. Davis, C. Coyle, M. Dandense, S.R., David, R., Delaney, K.R., Delgado, O., Denn, A.L., Ding, Y., Dink, H.H., Doulwalte, K.J., Draper, H., Dugan-Rocha, S. Euspin, K.J., Earthart, C. Edgar, D. Elwards, C.C., Elfaj, C., Escotto, M., Falls, T. Cergar, D. Elwards, C.C., Elfaj, C., Escotto, M., Falls, T. Garcia, M. Haviak, P. Hawis, C., Hamilton, K. Harris, C., Harris, K., Harris, K., Harris, K., Harris, K., Harris, C., Harris, K., Harris, C., Harris, K., Harris, K., Harris, K., Harris, C., Louse, M., Hollins, B., Homs, J., Holly, S., Klaan, U., Koran, J., Jackson, L., Li, J., Koran, J., Koran, J., Kovar, C., Kralsson, E., Martinez, E., Martinez, E., Martinez, E., Martinez, E., Massey, E., Mawhiney, E., Martin, R., Maylen, M., Martin, M., Massey, E., Mawhiney, E., Machell, H., Mohabat, K., Molyen, M., Morris, S., Gonh, M., Morris, S., Gonh, M., Orwnon, G., Conh, M., Orwnon, G., Chan, M., Orwnon, G., Chan, M., Orwnon, G., Chan, M., Orwnon, G., Chan, M., Chan, C., Chan, C., Chan, M., Chan, C., Chan, C.
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Submitted (31-JUL-2002) Human Genome Sequencing Center, Department
Submitted (31-JUL-2002) Human Genetics, Baylor Colisign of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
On Jul 23, 2002 this sequence version replaced gi:21914537.

Center: Baylor College of Medicine
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* (see http://www.hgsc.bom.tmc.edu/docs/Gennank_draft_data.html).
* NOTE: This is a "working draft' sequence. It currently
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   Alsbrooks, S.L., Amaratunge, H.C., Are, J.R., Ayele, M., Banks, T.,
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Worley, K.C.
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Rattus norvegicus clone CH230-6D13, *** SEQUENCING IN PROGRESS ***,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertabrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognatii; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DD 57359 IGCTTCAGCTGACCTTTCTCTCTAGACTGAGTTTTTGCTTGTTTTTGTCTTC 57340
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Musny, D.M., Adams, C., Adio-Oduola, B., Ali-osman, F.R., Allen, C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NOTE: This is a 'working drait' sequence. It currently consists of 3 contigs. The true order of the pieces is not known and their order in this sequence record is
                                                                                                                                                              Sequencing vector: plasmid; 100% of reads Chemistry: Dye-primer ET: 0% of reads chemistry: Dye-primer ET: 0% of reads chemistry: Dye-primer ET: 0% of reads assembly program: Phrap; version 0.990315 consensus quality: 171032 bases at least Q40 consensus quality: 171208 bases at least Q30 consensus quality: 171301 bases at least Q20 lineart size: 128000; agarose-fp insert size: 171876; aum.of-contigs Quality coverage: 12.05 in Q20 bases; sum-of-contigs Quality coverage: 12.05 in Q20 bases; sum-of-contigs
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92836: contig of 56480 bp in length
92936: gap of unknown length
172076: contig of 79140 bp in length.
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36357, 92886
/note-"assembly_name:Contig29"
92937, 172076
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Project Information
                                                                                                  Sequencing vector: M13; 0%
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/db_xref="taxon:10090"
                              Center project name: M_BB0157P05
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E 3 (bases 1 to 14810)

Birren, B., Initon, L., Nusbaum, C., Lander, E., Ali, A., Allen, N., Anderson, S., Barna, N., Bastien, V., Bloom, L., Boyuslavdy, L., Anderson, S., Barna, N., Bastien, J., Camapophano, A., Chagelo, Chazaro, B., Choppel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P., Cooke, P., Dehrellano, K., Dewark, Diala, J.S., Dodge, S., Farceira, P., Dehrellano, K., Dewark, Diala, J.S., Dodge, S., Gord, S., Goyette, M., Graham, L., Grand-Pierre, N., Gardyn, J., Glingo, J., Callins, S., Collymore, A., Karatas, A., Kalteugh, M., Illev, L., Johnson, R., Jones, C., Kamet, A., Karatas, A., Kalls, C., Levine, R., Lindblad-Toh, K., Liu, G., MacChand, P., MacQuis, N., Matchews, C., Macdonald, P., Major, J., Marquis, N., Matchews, C., Mihova, T., Menga, V., Murphy, T., Naylor, J., Naylor, C., Nicol, K., Norbu, C., Norman, C.H., O'Connor, T., O'Donnell, P., O'Neil, D., Olliver, J., Peterson, K., Phunkhang, P., Pierre, N., Pollara, V., Raymond, C., Retta, R., Pabeack, M., Riley, R., Rise, C., Rogov, P., Raymond, C., Retta, R., Yangen, S., Schauer, S., Schubback, R., Strauss, N., Subramanian, A., Talanga, T., Tesigye, S., Theodore, T., Volna, G., Vall, R., Waylen, Y., Young, G., Vall, R., Young, G., Vall, R., Waylen, Y., Young, G., Vall, R., Waylen, Y., Young, G., Vall, S., Calanoun, J., Zembek, L., Zimmer, A. and Zody, M., Vell, R., Voung, G., Collins, C., Collin E (bases 1 to 14810)

Birren, B., Linton, L., Nusbaum, C., Lander, E., Ali, A., Allen, N., Anderson, S., Linton, L., Nusbaum, C., Lander, E., Boyaslavkiy, L., Boukhgaller, B., Barna, N., Bastien, V., Bloom, T., Boyaslavkiy, L., Changaller, B., Choepel, Y., Canarale, J., Canapoplano, A., Chang, J., Chararo, B., Choepel, Y., Calangelo, M., Collins, S., Collymore, N., Cook, A., Cooke, P., DeArellano, K., Dewar, K., Dilez, J.S., Dodge, S., Faro, S., Ferreitz, P., Fitchugh, W., Gage, D., Galagan, J., Dodge, S., Goyette, M., Graham, L., Grand-Pierre, N., Gardyna, S., Goyette, M., Graham, L., Grand-Pierre, N., Canders, T., Lehoczky, J., Levine, K., Lamazeres, R., Landers, T., Lehoczky, J., Levine, R., Indibiad, Toh, K., Ilu, G., Macharo, C., Macdonald, P., Marquis, N., Matchess, C., Macdonald, P., Marquis, J., Marchess, C., Macdonald, P., Marquis, J., Narus, C., Nocer, M., McKernan, R., Marquis, J., Narus, C., Nocel, J., Nothu, C., Norman, C.H., O'Connor, T., O'Connor, T., O'Connor, T., O'Connor, T., O'Connor, T., Chonnell, P., O'Mail, D., O'Connor, T., O'Connor, T., Chonnell, P., O'Mail, D., O'Connor, T., O'Connor, T., Chonnell, P., O'Mail, D., O'Connor, T., Chonnell, P., O'Mail, D., Norway, T., Raymond, C., Retta, R., Rieback, M., Riley, R., Rise, C., Rogor, P., Senama, J., Rosetti, M., Tavis, R., Senaman, B., Severy, P., Spencer, B., Stange-Ihomann, N., Stojacoric, N., Viel, R., Vo.A., Wilson, B., Wux, Wayman, J., Yassillev, H., Zinmer, A. and Zody, M., Zwins, M., Travers, M., Tr Castle, A., Cerny, J., Colangelo, M., Collins, S., Collymore, A., Cooke, P., DeArellano, K., Depayre, E., Devon, K., Dewar, K., Donelan, L., Doyle, M., Ferreira, P., Fitzhugh, W., Forrest, C., Funke, R., Gage, D., Galagan, J., Gardyna, S., Gilbert, D., Grant, B., Hagos, B., Heaford, A., Horton, L., Howland, J. C., Jones, C., Kann, L., Kartaras, A., Lehoczky, J., Lieu, C., Locke, K., Macdonald, P., Marquis, N., MoEwan, P., McGurk, A., MoKernan, K., McChaughlin, J., Molla, M., Morris, W., Morrow, J., Mychalecky, J., Navlor, J., Niloff, M., O'Connor, T., O'Donnell, P., Pavlin, B., Peterson, K., Pollara, V., Riley, R., Roberts, D., Roy, A., Seyer, P., Stange-Thomann, N., Stojanovic, N., Stone, C., Subramanian, A., Parsiye, T., Charange, S., Torruella-Miller, I., Vassillev, H., Vo, A., Kagner, A., Andrew, A., Magner, A., Andrew, A., Andrew Direct Submission Submitted (28-JUL-1999) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA Submitted (22-MAR-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA Submitted (24-MAR-2002) Whitehead institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, 05A On Mar 24, 2002 this sequence version replaced 91:18640683. Wheeler, J., Wu, X., Wyman, D., Ye, W.J. and Zody, M. All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997) Direct Submission REFERENCE AUTHORS TITLE JOURNAL TITLE JOURNAL JOURNAL REFERENCE AUTHORS COMMENT

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Center: Whitehead Institute/ MIT Center for Genome Research.
Center code: WIBR
                             Web site: http://www.seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
..........Project Information
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/clone_lib-"RPCI-11 Human Male BAC"
344. .1086
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complement(2593. .2901)
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466. .5560
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:4642. .14673
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745. .5033
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076. .5193
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14590. .14625
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15048. .15355
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1732. .12008
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233. .5528
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SEQUENCE, 6 ordered pieces.
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1 25311: contig of 25311 bp in length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  39630 39729: gap of 100 bp 39730 48802: contig of 9073 bp in length 48903 48902 97214: contig of 22312 bp in length 71215 71314: gap of 100 bp 100 bp 71315 81533: contig of 10219 bp in length 81534 81533: gap of 100 bp 81534 81533: gap of 100 bp 81534 81533: gap of 100 bp 71315 91534: contig of 44481 bp in length 81534 81533: gap of 100 bp 81534 81533: gap of 100 bp 91534 81534 81534 81534 81534 81534 81534 81534 81534 81534 81534 81534 81534 81534 81534 81534 81534 81534 81534 81534 81534 81534 81534 81534 81534 81534 81534 81534 81534 81534 81534 81534 81534 81534 81534 81534 81534 81534 81534 81534 81534 81534 81534 81534 81534 81534 81534 81534 81534 81534 81534 81534 81534 81534 81534 81534 81534 81534 81534 81534 81534 81534 81534 81534 81534 81534 81534 81534 81534 81534 81534 81534 81534 81534 81534 81534 81534 81534 81534 81534 81534 81534 81534 81534 81534 81534 81534 81534 81534 81534 81534 81534 81534 81534 81534 81534 81534 81534 81534 815
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    74: gap of 100 bp 33568: contig of 3694 bp in length
                                                                                                                                                                                           25312 25411: gap of 100 bp
25412 25389: contig of 978 bp in length
26590 26489: gap of 100 bp
26490 227297: contig of 808 bp in length
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/clone_lib="RPC1-11 Human Male BAC"
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26490, 27297
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/note-"assembly_fragment"
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126215. .159223
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/db_xref="taxon:9606"
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Gardyna's. Gord's. Graham, L., Grand-Pierre, N., Hagos, B., Horton. Hume, W., Illev, I., Johnson, R., Jones, C., Kamat, A., Kalas, A., Kells, C., Landers, T., Lindblad-Toh, K., Lindblad-Toh, K., Lindblad-Toh, K., Lindblad-Toh, K., Lindblad-Toh, K., MacLean, C., Macdonald, P., Major, J., Matchews, C., Mornan, C., Mornan, C., Murphy, I., Major, J., Maneus, L., Minova, T., Mienga, V., Murphy, I., Major, J., Mayen, C., Nicol, R., Nicku, C., Norman, C.H., O'Connor, I., Yo'Donnell, P., O'Neil, D., Oilver, J., Peterson, Phunkhang, P., Peterson, Rayen, C., Rogov, P., Roman, J., Roy, A., Schauer, S., Schupbeck, R., Schamen, S., Severy, P., Smith, C., Spencer, B., Stange-Thoman, N., Sic, Sackie, R., Ralanas, J., Iestaye, S., Iheodore, J., Iopham, K., Itavers, M., Vassiliev, H., Vola, Wilson, B., Wu, M., Wyman, D., Young, G., Zalnoun, J., Peterson, J., Zimmer, A. and Zody, M.
AC129527 208010 bp DNA linear HTG 06-AUG-2002 HTGL 8apiens chromosome 17 clone RP11-95918 map 17, WORKING DRAFT
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Sutmitted (36-AUG-2002) Whitehead Institute/Wil Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
All repeats were identified using RepeatMasker:
Smit, A.E.A. & Green, P. (1966-1967)
                                                                                                                                                                                                                                                                                                                                                              Eukaryota, Metazoa, Chordata, Craniata, Verteurata, Euteleostomi,
Manmalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
1 (bases 1 to 208010)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Birten, B., Nusbaun, C., Lander, E., Ali, A., Aller, N., Anderson, S., Barren, B., Bastlen, V., Bloom, T., Boguslavkiy, L., Soukhgalter, B., Camarta, J., Charg, J., Chara, B., Cheepel, Y., Collymore, A., Cock, A., Cooke, P., Dehrellano, K., Dewar, K., Diaz, J.S., Dodge, S., Farco, S., Ferreira, P., FitzGerald, M., Gage, D., Galagan, J.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  * NOTE: Inis is a 'working draft' sequence, it currently consists of 6 contigs. Gaps between the contigs * are represented as runs of N. The order of the pieces
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Insert size: 207310; sum-of-contigs
Ousilty coverage: 13.6 in Q20 bases; agarose-fp
Quality coverage: 13.3 in Q20 bases; sum-of-contigs
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Sequenciar vector: Plasmid, n.d.: 100% of reads
Sequenciar Dye-terminator Big Dye; love of reads
Assembly program: Phrap, version 6.960731
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Web Site: http://www.seq.wi.mit.edu
Contact: sequence_submissions/gencie.wi.mit.edu
Contact: sequence_submissions/gencie.wi.mit.edu
Center project name: 127508
Center clone name: 959_1_8
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                                                                                                                                                                                                                              HIG: HIGS_PHASE2; HIGS_DRAFI; HIGS_FULLIOP.
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100 Lp

33463 33562: gap of

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contig of 11507 bp in length gap of unknown length contig of 11823 bp in length.
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Sairren, B., Linton, L., Nusbaum, C., Lander, E., Ailen, N., Anderson, S., Barra, N., Bastlen, V., Boguslavkiy, L., Boukhailer, B., Hrown, A., Camarata, J., Checkell, Y., Campoplano, A., Chang, J., Checkell, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Dewar, K., Dada, S., Collymore, S., Caro, Perretra, P., Fitchugh, W., Gage, D., Galagan, J., Gardyna, S., Ginde, S., Goyette, M., Graham, L., Grand, Pierre, M., Hagos, B., Hachord, A., Horton, L., Hulme, W., Lamazares, R., Landers, I., Lehcozky, J., Levine, R., Lin, G., Machen, K., Morener, R., Marquis, M., Mitthes, C., Machin, M., Matthews, C., Morent, L., Millova, I., Menga, V., Murphy, I., Naylor, S., Maymord, C., Norman, C.H., O'Connor, I., O'Connor, I., O'Connor, I., O'Connor, V., Peirre, N., Pollara, V., Raymord, C., Pererson, K., Phinn, Pollara, V., Raymord, C., Pererson, V., Peirre, N., Pellara, V., Raymord, C., Pererson, V., Pellara, V., Pellara
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Homo sapiens chromosome 17 clone RP11-95918 map 17, LOW-PASS
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Mammalia: Eutheria; Primates; Catarrhin; Hominidae; Homo.
1 (bases 1 to 853)
Birren, B., Linton, L., Nusbaum, C. and Lander, E.
Homo sapiens chromosome 17, clone RFII-95918
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Direct Submission
Submitted (25-MAR-2001) Whitehead Institute/MII Center for Genome Research, 320 Charles Street, Cambridge, MA 52141, USA
SALI reposts were identified Using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1957)
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                                                                                                                                                                                                                                                    34.7%; Score 35; DB 2; Length 125971; 66.7%; Pred. No. 9.8;
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Web site: http://www-seq.wi.mit.edu
/organism="Rattus norvegicus"
/db_xrefx="kaxon:10116"
/clone="CH330-270&15"
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Center clone name: 959_I_8
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* NOTE: This record contains 10 individual

FEATURES

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Sequencing vector: Plasmid;
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2 (bases 1 to 119207)
Worley, K.C.
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Rattus norvegicus clone CH230-452A23, *** SEQUENCING IN PROJEESS
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae,
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Muzny,D.M., Addans,C., Adio-Oduoia,B., Ali-osman,F.R., Allen,C.,
Alsbrooks,S.L., Amaratunge,H.C., Are,J.R., Ayele,M., Banks,I.,
Barbaria,J., Benton,J., Bimage,K., Blankenburg,K., Bonnin,D.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                consists of 14 contigs. The true order of the pleces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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163391: gap of unknown length
319378: contig of 155987 bp in length.
                                                                                                                                                          contig of 2396 bp in length.
gap of unknown length.
contig of 3883 bp in length.
gap of unknown length.
contig of 5218 bp in length.
gap of unknown length
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contig of 10815 bp in length
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contig of 4490 bp in length
gap of unknown length
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Matches 52; Conservative
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Buck, J., Bowle, S., Brieva, M., Brown, E., Brown, M., Bryatt, N.P., Buray, C., Burch, P., Burch, F., Byrd, N.C., Carter, C., Burrell, K.L., Byrd, N.C., Carter, M., Carter, S., Chacko, J., Chavez, D., Chen, S., Chen, R., Chen, C., Chonghay, I., Christopoulos, C., Clereland, C.D., Cox, C., Coyle, M.D., Dathorne, S.R., David, R., Davla, M.R., Davids, C., Dan, A.L., Ding, Y., Dinh, H.H., Delagdo, O., Denn, A.L., Ding, Y., Dinh, H.H., Delagdo, O., Denn, A.L., Ding, Y., Dinh, H.H., Barnarie, K.J., Draper, H., Dugan-Rocha, S., Curbin, X.J., Fariar, G., Edgor, D., Escotto, M., Fariar, I., Ferraguco, D., Flagg, M., Ford, J., Foster, P., Frantz, P., Gabis, A., Garcia, C., Elajo, C., Escotto, M., Harlandez, D., Harlandez, M., Kally, S., Euis, S., Cucari, S., Karisson, E., Kally, S., Khan, U., King, L., Korrak, J., Kursh, M., Martinez, E.,                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (see http://wrw.hgsc.bom.tmo.edu/docs/Gencank_drsft_data.html).
hOld: This is a "working draft' sequence, it currently
consists of 34 contigs. The true order of the pieces
is not known and their order in this sequence record is
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (19-JUL-2002) Human Genome Sequenciny Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, 1X 77030, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          * NOIE: Estimated insert size may differ irom sequence length
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Reb Site: http://www.hgsc.bom.tmc.edu/
Contact: hgsc-help@bom.tmc.edu
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Center clone name: CH230-452A23
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NOTE: This is a "working draft" sequence. It currently consists of 49 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N. but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                     Submitted (12-JUL-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, Tx 77030, USA 3 (bases 1 to 125703) Worley K.C.
Direct Submission
                                                                                                                                                                             Sequencing vector: Plasmid;
Sequencing vector: Plasmid;
Assembly program: Phrap; version 0.990325
Consensus quality: 84206 bases at least 040
Consensus quality: 94427 bases at least 030
Consensus quality: 96014 bases at least 030
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                                                                                                                       Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc.help@bcm.tmc.edu
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                                                                                         Center: Baylor College of Medicine
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score:	Sciring table: IDENTITY_NUC Scirched: Gapop 10.0 , Gapext 1.0 Scirched: 16154066 seqs, 8097743376 residues Tal number of hits satisfying chosen parameters: 32308132 Minimum DB seq length: 0 Miximum DB seq length: 0 Miximum DB seq length: 2000000000 Pist_processing: Minimum Match 0% Listing first 45 summaries	f.* em_estba:* em_esthum:* em_esthum:* em_esthum:* em_estpu:* em_estpu:* em_estpu:* em_htc:* gb_est1:* gb_htc:* gb_est2:* gb_est3:* gb_est3:* gb_est3:*	15: em_estfun:* 16: em_cstom:* 17: qb_gss.* 18: em_gss.hum:* 19: em_gss_lnv:* 20: em_gss_lnv:* 21: em_gss_lnv:* 21: em_gss_lnv:* 22: em_gss_fun:* 23: em_gss_fun:* 24: em_gss_fun:* 25: em_gss_fun:* 27: em_gss_pro:* 26: em_gss_pro:*	Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution. Submaries ** ** ** ** ** ** ** ** **

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Sawai, J., Shirayawa, A., Shibata, K., Yoshico M., Itoh, M., Ishii, Y., Arakawa, T., Hara, A., Fukunishi, Y., Kono, H., Adachi, J., Fukuda, S., Arakawa, T., Tawa, M., Nishi, K., Kivosa, H., Kodo, S., Yamanaka, I., Salto, T., Okazaki, Y., Okazaki, Y., Dibo, H., Kashawa, I., Saito, R., Kadora, K., Matsuda, H., Ashburner, M., Batacris, S., Casavari, T., Fleischmann, W., Basterland, T., Gissi, C., Kirj, E., Kochiwa, H., Kuehi, P., Leris, S., Matsuda, T., Gissi, C., Kirj, E., Kochiwa, H., Kuehi, P., Leris, S., Matsudi, T., Standi, C., Fucile, M., Nashio, T., Sakai, K., Okido, I., Furno, M., Aono, H., Baldrelli, R., Barsh, G., Blake, J., Boffeilli, F., Bojunga, M., Elecher, C., Fujtta, M., Cariboldi, M., Ostincich, S., Hill, D., Hercher, C., Fujtta, M., Cariboldi, M., Ostincich, S., Hill, D., Harolloni, L., Mashima, Y., Mazarelli, M., Sasaki, H., Saka, M., Lee, M., Hume, D.A., Kaniya, M., Lee, M., Lyons, F., Nordone, P., King, B., Ringwald, M., Rodriguez, I., Sakanolo, M., Sasaki, H., Sack, K., Wang, K.H., Weitz, C., Whittaker, C., Wilming, L., Warskaw-Boris, A., Yoshida, K., Hassegawa, Y., Kawaji, H., Kohtsuki, S., and Hayadhizki, Y., Matsuki, K., Mang, M., Hassegawa, Y., Kawaji, H., Kohtsuki, S., and Hayadhizki, Y., Wang, K.H., Maitz, C., Milming, L., And Mayanolo, M., Masagawa, Y., Kawaji, H., Kohtsuki, S., and Hayadhizki, Y., Wang, K.H., Maitz, C., Wang, K., Kawaji, H., Kohtsuki, S., and Hayadhizki, Y., Wang, K.H., Masagawa, Y., Kawaji, H., Kohtsuki, S., and Hayadhizki, Y., Wang, K.H., Masagawa, Y., Kawaji, H., Kohtsuki, S., and Hayadhizki, Y., Masagawa, Y., Kawaji, H., Kohtsuki, S., and Hayadhizki, Y., Rang, W., Kawaji, H., Shibada, M., Shibada, M., Shibada, S., Shiba
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                                                                               HTC 19-JAN-2002
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                                                                 AKO04721

Mus musculus adult male lung cDNA, RIKEN ruli-length enriched library, clone:1200012B22:FMS-like tyrosine kinase 1, full insert
                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Verteszata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognatni; Muridae; Murinae; Mus
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                                                                                                                                                                                                                                                                                                          Mus musculus (strain:C57BL/63) aduit male lung obnA to mRNA, clone_lib:RIKEN full-length enriched mouse cENA library
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HIC; CAP trapper.
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mRNA linear EST 23-D-C-1998
mm09f03.y1 Stratagene mouse diaphragm (#937303) Mus musculus CDNA
clone IMAGE-521021 5' similar to gp:X51602_cds1 VASCULAR
ENDOTHELIAL GROWTH FACTOR RECEPTOR 1 (HDNAN): gb:107297 Mus
musculus receptor tyrosine kinase (MOUSE);, mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mus musculus
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleosicani,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
1 (bases 1 to 855)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: mouseest@watson.wustl.edu
This clone is available foyalty-free through LLNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
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126 CCAAGAGCGACGTGTGGTCTTACGGAGTATTGCTGTGGGAAATCTTCTCCTTAGG 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Washington University School of Mediciner
4444 Forest Park Parkway, Box 8501, St. Louis, MG 63103
Tel: 314 286 1800
Fax: 314 286 1810
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89.6%; Pred. No. 2e-18;
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Contact: Marra M/Mouse EST Project
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/organism="Mus musculus"
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/clone="IMAGE:521021"
/clone_lib="Stratagene
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                                                                                                                                                                                                 CNS046JU 888.bp DNA linear GSS 21-MAY-2000 Tetraodon nigroviridis genome survey sequence PUC-Ori end of clone 104812 of library G from Tetraodon nigroviridis, genomic survey
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This sequence is a single read and was generated as part of a large scale clone-end sequenciny project of the Terrasdon nigroviridis genome. For more information, please take a losk at
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Actinopterygii; Neopterygii; Teleostei; Eutelecstei; Neotelecstei;
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Tetraodon nigroviridis DNA sequence
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/db_xref="taxon:99883"
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Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the foliowing URL (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=st2=PM1-HT0452-070 900-010-c02st3=2000-09-07st4=1)
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//foce="Organ: head_neck; Vector: pucl8; Site_1: Smal;
Site_2: Smal; A mini-library was made by cloning products
derived from ORESIES PK (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the pUC 18 vector. Reverse transcription of
tissue mRNA and CNA amplification were performed under
                                                                                                                                                                                                                                 Dias Neto, E., García Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsakuma, A., Bala, G.S., Simpson, D.H., Brunstein, A., deblivala, P.S., Bucher, F., Jörgeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., Jörgeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., Jörgeneel, C.V., O'Hare
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Laboratory of Cancer Genetics
Ludvig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01503-010, Sao Paulo-SP,
                                                                                                                                                Eukaryota, Metazba, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Mammalia, Eutheria, Primates, Catarrhin; Hominidae, Homo.
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BG461750 Athersys RAGE Library Homo sapiens SENA, mRNA Sequence.
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80.5%; Pred. No. 6e-13;
tive 0; Mismatches 22;
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162 c 132 g 163 t
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/db_xref="taxon:9606"
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High quality sequence start: 18
High quality sequence stop: 575.
Location/Qualitiers
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Fax: +55-11-2707001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleosicmi,
Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nurakami, Y., Li, H., Chowdhury, S., Yamada, K.M. and Yamada, Y.
EST sequences from E8.5 mouse craniofacial obna library
Unpublished (2000)
Contact: Yoshiniko Yamada
Craniofacial Developmental Biology and Regeneration Branch
Mational Institute of Dental and Craniofacial Research
9000 Rockville Pike, Building 30, Room 405, NIDGR, WIH, Bethesda,
                                                                                                                                                         69 CICGACITCCICIGAAATGGATGGCTCCTGAATCIATCITTGACAAAATCIACAGCACCA 128
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                                                                          DB 13; Length 689;
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Pred. No. 3.9e-12;
0; Mismatches 23;
(Wellcome/CRC Institute). "
135 c 167 g 171 t
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/clone="EGS992"
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79.5%;
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Fax: 301 402 0897
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RESULT 13 66577273

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encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library, Genome Res. 11 (2), 281-289 (2001) Kondo,S., Shinagawa,A., Salto,T., Kiyosawa,H., Yamanaka,I., Aizawa,K., Pukuda,S., Hara,A., Itoh,M., Kawai,J., Shitata,K. and Hayashizaki,Y. and Computational Analysis of Full-Length Mouse cDNAs Compared with Human Genome Sequences Mann. Genome. 12, 673-677 (2001) Please visit our web site (http://genome.gsc.riken.go.jp/) for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Arakawa,I., Carninci,P., Fukuda,S., Furunc,M., Hanagaki,T., Hara,A., Hiramoto,K., inofi,F., Ishii,Y., TLO,M., Kavai,J., Konoo,H., Kouda,M., Koya,S., Marsuyama,I., Miyazaki,A., Nomica,K., Ohno,M., Okazaki,Y., Okido,I., Saito,R., Sakai,C., Sakai,K., Sano,H., Sasaki,C., Sakai,K., Sano,H., Sasaki,C., Sakai,K., Sano,H., Sasaki,C., Sakai,K., Sano,H., Sasaki,M., Tagawa,A., Shiraki,T., Sogabe,Y., Suzuki,H., Muramatsu,M., and Hayashizaki,F., Takeda,Y., Tanaka,T., Toya,T.,
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URL:http://genome.go.criken.go.jp,
URL:http://genome.go.criken.go.jp/
Carninci.P., Shibata,Y., Hayatsu,W., Suganara,Y., Shibata,K., Itoh
,M., Kondo,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cONs libraries for rapid discovery of new
genes. Genome Res. . 10 (10), 1617-1630 (2000)
wagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E.,
Watahiki,M., Yoneda,Y., Ishikawa,I., Ozawa,K., Tanaka,I., Matsuura
Hayashizaki,Y.
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                 EST 26-0CT-2001
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                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazca; Chordata; Craniata; Vertebrata; Euteleostomi;
Manmalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 656)
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BB577273 KIKEN full-length enriched, 14 days embryo thymus Mus musculus cDNA cione 613040107 5', mkNA sequence.
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Contact: Yoshihide Hayashizaki
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Unpublished (2001)
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/dev_stage="14 days embryo"
/lab_host="DH108"
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/strain="C57BL/6J"
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Location/Qualifiers
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Fax: 81-45-503-9216
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December 8, 2002, 07:10:23 ; Search time 75:3682 Seco..ds (without alignments) 1478.802 Million cell updates/sec
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cgn2_6/ptodata/1/pubpna/US10_PUBCOMB.seq:*

/cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:*

/cgn2_6/ptodata/1/pubpna/Us60_PUBCOMB.seq:*
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/cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
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/cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*
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/cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:
GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.
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Listing first 45 summaries
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Gapop 10.0 , Gapext 1.0
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Maximum DB seq length: 2000000000
                                                                                                                                                                                                                                                                               Title:
Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Database :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Searched:
                                                                                                                                                                                                                                                                                                                                           Sequence:
                                                                                                                                                                     Run on:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

			Description		Sequence 5, Appli			i C	. . m			7	ur,		0.87		Sequence . Appli		1, 1	(*-	ري	ur.	ò	:
SUMMARIES			ID		US-09-919-408-5	US-09-872-136-5	US-09-766-678-1	US-09-982-610-22	US-09-919-408-3	US-09-872-136-3	US-09-982-610-31	US-09-982-610-17	US-09-982-610-45	US-09-866-510-21	US-09-960-352-10875	US-09-960-352-1177	US-09-866-510-1	US-09-866-510-3	US-09-866-510-5	US-09-866-510-7	US-08-866-510-9	US-09-955-363-35	US-09-919-497-40	
			DB		10	10	10	10	10	10	10	10	10	10	10	10	10	10	10	10	10	5	10	
			Match Length DB		5406	5406	5470	3120	3501	3501	4425	6827	9108	3321	332	355	3270	3270	3270	3270	3270	4054	6378	
	æ	Query	Match	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	24.8	24.8	24.8	22.3	22.3	22.3	21.8	21.8	21.8	21.7	21.7	21.7	21.5	21.5	21.5	21.5	21.5	21.5	21.5	
			Score	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	74.6	74.6	74.6	67.2	67.2	67.2	65.6	65.6	65.6	65.4	65.2	65.2	64.8	64.8	64.8	64.8	8.40	64.8	64.8	
		Result	NO.			2	e	₹*	'n	Ø	7	ဆ	ō	10	c 11	c 12	13	14	15	16	17	18	6 E	

sequence 1, Appli Sequence 15, Appl Sequence 17, Appl Sequence 19, Appl Sequence 10878, A Sequence 10878, A Sequence 2603, A Sequence 4293, A Sequence 1442, A Sequence 271, Appl Sequence 271, Appl Sequence 271, Appl Sequence 271, Appl Sequence 1399, Appl Sequence 1399, Appl Sequence 1399, Appl Sequence 1399, Appl Sequence 177, Appl Sequence 1789, Appli Sequence 1789, Appli Sequence 277, Appli Sequence 277, Appli Sequence 278, Appli	EM CELL
0 US-09-765-587-1 0 US-09-866-510-13 0 US-09-866-510-15 0 US-09-866-510-17 0 US-09-966-510-19 0 US-09-960-352-2603 0 US-09-960-352-2603 0 US-09-960-352-108-78 0 US-09-960-352-11442 0 US-09-960-352-11442 0 US-09-960-352-11442 0 US-09-960-352-11442 0 US-09-960-352-1442 0 US-09-960-352-1442 0 US-09-960-352-146-159-9 0 US-09-960-354-456-159-9 0 US-09-960-352-8227 0 US-09-960-352-8227	GUMENTS GUMENTS HEMATOPOIEIIC SI AND THEIR LIGANDS Incorporated #S-DOS # 1.0, Version # # 1
221.2 221.2 221.2 221.2 221.2 221.2 221.2 221.2 221.2 221.2 221.2 23.3 2	Tation US/ Icanischka Icanis
010 020 020 020 020 020 020 020 020 020	SULT 1 -05-915-408-5 Sequence 5, Applice 5, Applice 6, Month 1 Tile 0F IN Tile 1 Til
o o 'o	M D C C C C C C C C C C C C C C C C C C

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APPLICATION NUMBER: US/09/919,408
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Best Local Similarity
Matches 96; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2648 CACITGGT 2655
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         174 CCTIAGGT 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-919-408-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   69 CICGACTICCICIGAAAIGGAIGGCICCIGAAICIATCITIGACAAAAICIACAGCACCA 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Tsai, Shoo Ping Mood, William I.
TITLE OF INVENTOR: PROPEIN TYROSINE KINASE AGONISI ANTIBODIES NUMBER OF SEQUENCES: 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         129 ASAGCGACGTGTGGTCTTACGGAGTATTGCTGTGGGAAATCTTCTCCTTAGGT 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 5470;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              24; Indels
                                                                                                                                                                                                                                                 SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION UNDER: US/09/766,678
FILING DATE: 25-Jan-2001
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 74.6; DB 10;
Pred. No. 1.8e-13;
                                    ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER: 7683-060
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STREET: 460 Point San Bruno Blvd CITY: South San Francisco
                                                                                                                                                              CCMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: 08/193,829
FILING DATE: 09-FEB-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CCATION: 286..4386
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Coruzzi, Laura A. REGISTRATION NUMBER: 30,742
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)790-9090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 22, Application US/09982610 Patent Nr. US20020146420A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Lee, James M.
Matthews, William
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 5470 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bennett, Brian D.
Goeddel, David
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: (212)869-9741
                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: nucleic acid
STRANDEDNESS: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEX: 66141 PENNIE INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ArPLICANT: Genentech, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 24.8%; 78.8%;
                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
                    CCRRESPONDENCE ADDRESS:
ADDRESSEE: Pennie
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STATE: California
NUMBER OF SEQUENCES: 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: unknown MCLECULE TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 78.85
Matches 89; Conservative
                                                                                                     STATE: New York COUNTRY: U.S.A.
                                                                                                                                              ZIP: 10036-2711
                                                                                 CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 4
US-09-582-110-22
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-766-678-1
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2588 GCAICIACACCATFAAGAGTGATGTCIGGTCATATGGAATAIIACTGIGGGAAATCTTCT 2647
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    54 TIGCCCICTICTAGACTCGACTTCCICTGAAATGGATGGCICCTGAATCTATCTTGACA 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             114 AAATCTACAGCACCAAGAGCGACGTGTGTGTCTTACGGAGTATIGCTGTGGGAAATCTTCT 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           22.3%; Score 67.2; DB 10; Length 3120; 70.3%; Pred. No. 2.9e-11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Lemischka, Ihor R. TILLE OF INVENTION: TOTIPOTENT HEMATOPOIETIC SIEM CELL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RECEPTORS AND THEIR LIGANDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
ADDRESSEE; ImClone Systems Incorporated
SIREET: 180 Varick Street
                                                                                                                                    CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/982,610
FILING DATE: 17-Oct-2001
CLASSIFICATION: «Unknown>
PRICK APPLICATION DATA:
APPLICATION DATA:
FILING DATE: 1596-MAY-23
APPLICATION NUMBER: 08/222616
FILING DATE: 04-APR-1954
ALIORNYYAGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                    NAME: Lee, Wendy M.
REGISTRATION NUMBER: 40,378
REFERENCE/DOCKET NUMBER: P0821P3PCT
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Mismatches
                                                                                             OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: WinPatin (Genentech)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ) SEQUENCE DESCRIPTION: SEQ ID NO: 22: US-09-982-610-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 3, Application US/09919408; Patent No. US20020072077A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IELEPHONE: 415/225-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 3120 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEX: 415/952-9881
TELEX: 910/371-7168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SIRANDEDNESS: Single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INFORMATION FOR SEQ ID NO: 22:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES: 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IYPE: Nucleic Acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
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3251 COCGGCIGCCCCIGAAGTGGATGGCCCCTGAAAGCATCTTCGACAAGGIGTACACCACGC 3310
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          69 CICGACIICCICIGAAAIGGAIGGCICCIGAAICTATCIIIGACAAAAICIACAGCACCA 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                            Isai, Siao Ping
Wood, William I.
TITLE OF INVENTION: PROTEIN TYROSINE KINASE AGONISI ANTIBODIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .
0
                                             2493 AGAGTGACGTGTGGTCCTTGGGGTGCTTCTGGGAGAICTTCTCTGGG 2442
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                129 AGAGCGACGIGTGGTCTTACGGAGTATTGCTGGGAAATCITCICCITAGG 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDIOW TYPE: 3.5 inch, 1.44 Mb floppy disk COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Winbalin (Genentech) APPLICATION DATA: APPLICATION NUMBER: US/09/982,610 FILMS DATE: 17-Oct-2001 CLASSIFICATION: <UNKNOWN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REGISTRATION NUMBER: 40,378
- REFERENCE/FOCKET NUMBER: P0821P3PCT
IELECOMGUNICATION INFORMATION:
TELEPHONE: 415/225-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: Linear SEQUENCE DESCRIPTION: SEQ ID NO: 17: US-09-962-610-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA: APPLICATION NUMBER: 08/446,648
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE: 1996-MAY-23
APPLICATION UNYBRE: 08/222616
FILING DATE: 04-APR-1594
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: Genentech, Inc
STREET: 460 Point San Brun
CITY: South San Francisco
                                                                                                                                                                                                  Sequence 17, Application US/09982610 Patent No: US26020146420A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                 Lee, James M.
Matthews, William
                                                                                                                                                                                                                                                                         Genentech, Inc.
Bennett, Brian D.
Goeddel, David
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: 415/952-9881
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRANDEDNESS: Single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO: 17:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        910/371-7168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ZIP: 94080
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES: 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Lee, Wendy M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: Nucleic Acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                      Genentech,
                                                                                                                                                                                                                                                                    APPLICANT:
                                                                                                                                                       RESULT 8
US-09-982-610-17/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 9
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                                                                   2645 GCATCTACACCATTAGAGTGATGTCTGGTCATATGCAATATACTGTGGGAAAICTICT 2704
                                                                                                                              114 AAAICTACAGCACCAAGAGCGACGTGTGGTCTTACGGAGTATTGCTGTGGGAAATCTTCT 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         69 CTCGACTTCCTCTGAAATGGATGGCTCCTGAATCTATCTTTGACAAAATCTACAGCACA 128
                                           54 TIGCCCICTICIAGACICGACTICCICTGAAAIGGAIGGCICCIGAAICIAICIIIGACA 113
      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: PROTEIN IYROSINE KINASE AGONIST ANITEODIES NUMBER OF SEQUENCES: 45
    0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ;
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    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       29; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
WEDIUW TYPE: 3.5 inch, 1.44 Mb floppy disk COMPUTER: IBM PC COMPUTED:
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatin (Genentech)
CURRENT APPLICATION DATA:
  38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 21.8%; Score 65.6; DB 10;
Best Local Similarity 74.1%; Pred. No. 1.1e-10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/09/982,610
FILING DATE: 17-Cct-2001
CLASSIPICATION: CUASSIPICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
FILING DATE: 1996-MAY-23
APPLICATION NUMBER: 08/222616
FILING DATE: 1996-MAY-24
APPLICATION NUMBER: 08/222616
ATICATION NUMBER: 08/222616
ATICATION PAPE: 04-APR-1954
ATICATION PAPE: 04-APR-1954
ATICATION PROPARATION:
NAME: Lee, Wendy M.
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    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STRRET: 460 Point San Bruno Blvd
CITY: South San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: Linear
SEQUENCE DESCRIPTION: SEQ ID NO: 31;
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REFERENCE/DOCKET NUMBER: P0
                                                                                                                                                                                                                                                                                                                                                               Sequence 31, Application US/09982610; Patent No. US20020146420a1
GENERAL INFORMATION:
APPLICANT: Genentech, Inc.
Geoddel, David
Lee, James M.
Matthews, William
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELECOMMUNICATION INFORMATION:
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TYPE: Nucleic Acid
STRANDEDNESS: Single
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Wood, William I.
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  Conservative
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IIILE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING FIBROTIC DISEASES FILE REFRENCE: ERM-104.01 CURRENT APPLICATION UNMER: US/09/866,510 CURRENT FILING DATE: 2001-05-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: KAZLAUGKAS, ANDRIUS
APPLICANT: IKUNO, YASUSHI
TITLE DE INVENTION: METHODS AND COMPOSITIONS FOR TREATING FIBROFIC DISEASES
FILE REFERENCE: EBM-10A NUMBER: US/09/866,510
CURRENT APPLICATION NUMBER: US/09/866,510
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75.0%; Pred. No. 1.7e-10;
tive 0; Mismatches 27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Search completed: December 8, 2002, 09:25:43 Job time : 98.3682 secs
                                                                     PRIOR APPLICATION NUMBER: 2001-05-25
PRIOR APPLICATION NUMBER: 60/250,747
PRIOR APPLICATION NUMBER: 60/280,103
PRIOR APPLICATION NUMBER: 60/289,103
PRIOR APPLICATION NUMBER: 60/289,103
PRIOR FILING DATE: 2001-05-07
NUMBER OF SEQ ID NOS: 33
SEQ ID NO 3
LENGIR: 3270
TUENGIR: 3270
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PRIOR FILING DATE: 2000-12-01
PRIOR APPLICATION NUMBER: 60/289,103
PRIOR FILING DATE: 2001-05-07
NUMBER OF SEQ ID NOS: 33
SOFTWARE: Patentin Ver. 2.1
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Best Local Similarity 75.07
Matches 81, Conservative
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Matches 81; Conservative
                                                                                                                                                                                                                                                                                                  IYPE: DNA
ORGANISM: Homo saplens
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ORGANISM: Homo sapiens
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; LOCATION: (1)..(3267)
US-09-866-510-3
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US-09-866-510-5
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APPLICANT: Mathialagan, Nagappan
TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
TITLE OF INVENTION: MUSCLE AND FAT DEPOSITION
FILE REFERENCE: 16511.006/37-21(10298)C
CURRENT APPLICATION NUMBER: US/09/966,352
CURRENT FILING DATE: 2001-09-24
NUMBER OF SEQ ID NOS: 15112
ENGTH: 355
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TITLE OF INVENTIONS METHODS AND COMPOSITIONS FOR TREATING FIBROTIC DISEASES
FILE REPERENCE: ERM-104.01
CURRENT RELIKO BATE: 2001-05-25
PRIOR APPLICATION NUMBER: 60/250,747
PRIOR APPLICATION NUMBER: 60/250,747
PRIOR FILING DATE: 2000-12-01
PRIOR FILING DATE: 2000-13-01
PRIOR FILING DATE: 2001-05-07
NUMBER OF SEQ ID NOS: 33
SEGTWARE: PALENTIN VET: 2.1
SEQ ID NO 1
LENGTH: 3270
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                                                                                                                                                                                                                                                                                                                                     Query Match
21.7%; Score 65.2; DB 10;
Best Local Similarity 74.5%; Pred; No. 4.7e-11;
Matches 82; Conservative 0; Mismatches 28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 1, Application US/09865510
Patent No. US20020111304A1
GENERAL INFORMATION:
APPLICANT: KAZLAUSKAS, ANDRIUS
APPLICANT: IKUNO, YASUSHI
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Patent No. US20020111304A1
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75.0%;
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APPLICANT: KAZLAUSKAS, ANDRIUS
APPLICANT: IKUNO, YASUSHI
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Best Local Similarity 75.09
Matches 81; Conservative
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US-09-866-510-1
                                                                                                                                                                                                                        TYPE: DNA ORGANISM: Bos taurus
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                        Sequence Market M
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Sequence 3
Sequence 1
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TILLE OF INVENTION: HUMAN RECEPTOR TYROSINE KINASE, KDR NUMBER OF SEQUENCES: 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM IYPE: Floppy disk
COMPUTER: IBM PC compalible
OPERATIVE SYSTEM: PC-DGS/MS-DOS
SOFIWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DAIA:
US-08-601-891-3
US-09-021-324-3
PCT-US92-05401-3
PCT-US92-09893-3
US-08-340-011-1
US-08-901-710-1
US-08-91-735-790-1
US-08-601-132-36
US-08-601-132-36
US-08-601-132-36
US-08-446-648-31
PCT-US95-04228-31
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PCT-US95-04228-17
US-08-446-648-45
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US-08-901-710-3
US-08-222-616-17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER: 19963PV TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: linear
MGLECULE FYPE: CDNA
SLQUENCE DESCRIPTION: SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Co., Inc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Hand, J. Mark
REGISTRATION NUMBER: 36,545
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   S-09-098-707A-1
Sequence 1. Application US/09098707A
Patost No. 6204011
GENERAL INFORMATION:
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Thomas, Kenneth A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEPHONE: 732/594-3905
TELEFAX: 732/594-4720
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LENGIH: 4071 base pairs
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SIREEI: P.O. BOX 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: nucleic acid
STRANDEDNESS: double
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US-07-977-451-5
US-07-946-507-3
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Copyright (c) 1993 - 2002
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                                                                                                                                                                                                      36786. 36959
7.00te="MER20 repeat: matches 2. 169 of consensus"
37212. 37318
70218- MIR repeat: matches 131. 241 of consensus"
70218- 37330
7020e="L2 repeat: matches 2688. 2739 of consensus"
7059. 37781
700te="FLAM_C repeat: matches 1. 125 of consensus"
           /note="MER5A repeat: matches 4. .189 of consensus" 32946. .33076
/note="FLAM.A repeat: matches 1. .133 of consensus" 33231. .33323
/note="MIR repeat: matches 118. .222 of consensus" 33433. .3347
                                                                                                                  hote="Aluxb8 repeat: matches 1. .313 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                         note="AluJo repeat: matches 86. .274 of consensus"
                                                                                                                                                                                                                                                                                                                                                     38866. 39047
/note="MER5A repeat: matches 1. 186 of consessus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                               40286. .40581
/Aote="Alusp repeat: matches 1. .297 of consensus"
41033. .41330
43786. .43971
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3786. 43971
'note="WER5B repeat: matches 1. .177 of consensus"
                                                                                                                                                     note-THEIB repeat: matches 1. .364 of consensus
15886 .36063
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Moote-"NHREA repeat: matches 8. .189 of consensus" (5327. .45508
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     note="MER3 repeat: matches 1, .193 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          39114. .39348
/note="MIR repeat: matches 4. .231 of consensus"
40010. .40203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               99.5%; Score 299.4; DB 9; Length 164519; 99.7%; Pred. No. 3.38-78; tive 0; Mismatches 1; Indels 0;
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/note="89 copies 2 mer tt 57% conserved"
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Mary D.M. Adams, C. Adio-Oduola, B., Ali-Osman, F.R., Allen, C., Autony, D.M., Adams, C., Adio-Oduola, B., Ali-Osman, F.R., Allen, C., Alixy, D.M., Adams, C., Adio-Oduola, C., Barken, C., Burkell, K.L. Byrd, N.C. Carter, M. Cavazos, S.R., Chacko, J. Chavez, D., Chen, Z. Chowdhry, J., Christopoulos, C., Carter, C., Burkell, K.L. Byrd, N.C. Carter, M. Cavazos, S.R., Chacko, J., Chavez, D., Carter, M., Cavazos, S.R., Chacko, J., Chavez, D., Carter, M., Cavaro, J., Charles, C., David, R., Davy-Carter, M. Douthwaite, K. J., Dapper, H., Dagan-Rocha, S. Lirbin, K.J., Douthwaite, K. J., Dapper, H., Dagan-Rocha, S., Darholl, H.H., Douthwaite, K. J., Dapper, H., Dagan-Rocha, S., Lirbin, K.J., Earnhart, C., Edgar, D., Flagg, N., Ford, J. Carter, M. Garner, T., Carta, M., Gill, R., Harris, C., Hodgson, A., House, M., Hawels, H., Harris, C., Harris, K., Harr, M., Havlak, P., Hawels, A., Harnandez, J., Homsi, J., Hollins, B., Harris, C., Hadgson, A., House, M., Hollins, B., Jackson, E., Marris, C., Huber, J., Hully, S., Hume, J., Jackson, L. E., Jackson, E., July, S., Man, U., King, L., Korrah, J., Licharage, M., Holloway, C., Hawi, G., Marrinez, E., Marrinez, Massey, E., Marrinez, E., Witchell, T., Mohabbat, K., Marz, S., Savery, G., Sodergren, E., Marrinez, M., Mauja, P., Marchell, M., Nalle, M., Nalle, M., Rapio, M., Mauja, P., Marrinez, M., Mauja, M., Marrinez, M., Marrinez, S., Marren, R., Marrington, S., Marren, R., Marrington, S., Marren, R., Marrington, S., Marren, R., Marrington, C., Wallington, S., Wallington,
พบเมชยงช์
Rattus norvegicus clone CH230-69N22, *** SEGÜENCING IN PROGRESS
***, 59 unordered pleces.
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Center: Baylor College of Medicine
                                                                                                                                                                                                                                                                                      Eukaryota; Matazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognatni; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Chemistry: Dye-terminator Big Dye: 100% of reads
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Consensus quality: 55655 bases at least Q40
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                                                                                                                                                                                                                     Rattus norvegicus,
                                                                                                                                                                                                                                                           Rattus norvegicus
                                                                                                                                                                                         HIG; HIGS PHASE1,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Direct Submission
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                                                                                                                        AC128808
                                                                                                                                                                                                                                                                                                                                                        Rattus.
                    LOCUS
DEFINITION
                                                                                                                                                                                                                                                    CHGANISM
                                                                                                                     ACCESSION
                                                                                                                                                   VERSION
KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AUTHORS
TITLE
                                                                                                                                                                                                                                                                                                                                                                                   KEFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                  AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                JCURNAL
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contig of 1318 gap of unknown	46200: contig of 1115 bp 146300: gap of unknown leng 47472: contig of 1172 bp 147572: gap of unknown leng 49428: contig of 1856 bp 14528: gap of unknown leng 5158: gap of unknown leng 5158: gap of unknown leng 5158: gap of inchnown leng	229 51528: gap of unknown length 529 52699: contig of 1171 bp in. 700 52799: gap of unknown length	54476: contig of 1677 bp in 54576: gap of unknown length 55910: confid of 1336 hm in	56012: gap of 57709: contig	57809: gap of unknown length 59789: contig of 1980 bp in		63284: contig of 1814 b	66086: contig of 2702 66186: gap of unknown	68110: contig of 1924 68210: gap of unknown	70567: contig of 2357 70667: gap of unknown	71935: contig of 1272 k 72039: qap of unknown 1	74045: contig of 2006 b	75300: contig of 1155 75400: dan of unknown	78074: contig of 2674 F	80451: Gap of unknown 1 80451: Contig of 2317 K 80551: gap of unknown 1	82240: Contig of 1649 E	85014: contig of 2674 85314: can of unknown	86906: contig of 1792 bp i 87006: gap of unknown leng	89570: contig of 2564 b		93811: contig of 1927 b	96213:	41.3%; Score 124.2; milarity 80.2%; Pred No. 4.3c	nes 158; Conservative 0; Mi		Db 30810 AAGGICCCAIGCTGITICCACACICGACTICCCCIAAAAGGALGGCICCCGAATCCAI 30751	. 97 106 CITTGACAAAATCIACAGCACCAAGAGGGACGTGTGGTTACGGAAJATIGCTGTGGGA 165 HILLIHIH HILLIHIH HILLIHIHIHIHIHIHIHIHI		
Consensus quality: 59929 bases at least Q30 Consensus quality: 62415 bases at least Q20	* NOTE: Estimated insert size may differ from sequence lengt: * (See http://www.hgsc.bom.tmc.edu/docs/Genbank draft_dats.itml). * NOTE: This is a 'working draft' sequence. It currently consists of 59 contigs. The true order of the pieces * is not known and their order in this sequence record is * arbitrary. Gaps between the contigs are represented as	ips are unkno Nished sequen Ssion number	1 1002: contig of 1002 bp in le 1003 1102: gap of unknown length	2129: contig of 1027 bp in le 2229: gap of unknown length	323/: CONTIG OF 1008 E 3337: gap of unknown 1 4784: CONTIG OF 1447 E	4884: gap of unknown length 5614: contig of 1730 bp in le	8257: contig of 1543 E	9307: gap or unknown 1 9401: contig of 1044 E 9501: gap of unknown 1	10661: gap of unknown 1 10761: contig of 1160 b	11930: contig of 1169	13552: contig of 1522	15262: contig of 1610	15302: gap or unknown length 16503: contig of 1141 bp in len	16603: gap of unknown length 17964: contig of 1361 bp in len	18064: gap of unknown length 19537: contig of 1473 bp in len	21165: contig of 1528	21265: gap of unknown length 22824: contig of 1559 bp in len	22924: gap or unknown length 23965: contig of 1041 bp in len	24065: gap of unknown len 25710: contig of 1645 bp	25810: gap of unknown length 27147: contig of 1337 bp in len	28860: contig of 1613 bp.	29963: gap of 29963: contig 30063: gap of	3123: contig of 1060 bp in len 31223: gap of unknown length	32967: gap of unknown length	34170: contig or 1103 bp in len 34170: gap of unknown length 36370: contig of 2200 bp in length	36470: gap of unknown length	3/801: contig of 1331 3/901: gap of unknown 39087: contig of 1186 3/9187: gap of unknown	of 1525 b unknown l of 1430 b	

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APPLICANT: Unmounter, Laure
APPLICANT: Londed, Jamila
APPLICANT: Londed, Jamila
APPLICANT: Londed, Jamila
APPLICANT: Renauld, Jean-Christophe
TILLE OF INVENTION: TSolated Nucleic Acid Molecules which Encode T Cell Inducibl
TILLE OF INVENTION: THE Proteins Encoded, and Uses Thereof
FILE APPLICATION NUMBER: US/05/354,243B
CURRENT FILENG DATE: 1999-07-16
PRICE FILING DATE: 1998-10-26
PRICE FILING DATE: 1998-10-26
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3058 ILCCIGACCAICALLTAATGAGTGTGACTGTTTCTTCCTTTGATAATTGAAGCTTTGTA 317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       39 IGCCI: IICCIG: CIIGAIAATICTITCIGTTCATTAGATAGTAAAIGCTTTCAA 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        27.5%; Score 27.8; DB 4; Length 4797; 65.1%; Pred. No. 7.3; 1ve 0; Mismatches 22; Indels 0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             M.DIUM TYPE: Floppy disk
C.MPUTER: IBM PC compatible
C.BRAITIN SYSTEM: PC-DOS/MS-DOS
S.FTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RICE ACTIN GENE AND PROMOTER 27
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION DATA:
A.PPLICATION NUMBER: US/08/144,602B
FILING DAIE: 27-007-1993
CLASSIFICATION: -536
                                                                                                                                                                                                        US-09-354-2438-25
; Sequence 25, Application US/09354243B
; Patent No. 6359117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 4, Application US/081446027
Patent No. 5641876
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTURNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: NGBLOY DAVID APPLICANT: Wu, F, TITLE OF INVENTIA: RICE A NUMBER OF SEQUEN SS. 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 27.5% Best Local Similarity 65.1% Matches 41; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQ ID NOS: 29
SEQ 1D NO 25
LENCIH: 4797
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COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          S.ALET: CLINES:
CITY: ROCHESTER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NEW YORK
                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
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                                                                                                            3118 GIT 3120
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                                                                                     99 GTT 101
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APPLICANT: Dumoutier, Laure
APPLICANT: Loubled, Jamila
APPLICANT: Soldated Nucleic Acid Molecules which Encode T Celi Inducible Fac
TITLE OF INVENTION: (TITES) The Proteins Encoded, and Uses Thereof
FILE REFERENCE: LUD 5543.2
CURRENT FILING DATE: 1999-10-18
PRIOR APPLICATION NUMBER: US09/354,243
PRIOR FILING DATE: 1999-07-16
PRIOR APPLICATION NUMBER: US09/354,243
PRIOR FILING DATE: 1999-07-16
PRIOR FILING DATE: 1998-10-26
NUMBER OF SEQ ID NOS: 29
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  27.5%; Score 27.8; DB 4; Length 4597; 59.5%; Pred. No. 7.2; Live 0; Mismatches 32; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            27.5%; Score 27.8; DB 4; Length 4797; 65.1%; Pred. No. 7.3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        32; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       22; Indels
                                                                                   COMPUTER TRADBLE FORM:
MEDUDY TYPE: Diskette, 3.50 inch, 1.4Mb storage
COMPUTER: HP Vectra 436/33
OPERATING SYSTEM: MSDOS Version 6.2

 Mismatches

                                                                                                                                                                                                                 US/08/961,527
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GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                         TELEPONE (301) 305-8504
TELEPONE (301) 305-8504
TELEPAR: (301) 309-8512
INFORMATION FOR SEQ ID NO: 175:
SEQUENCE CHARACIERISTICS:
  9410 Key West Avenue
                                                                                                                                                                                                                                                                                                                                ATIORNEY/AGENT INFORMATION:
NAME: Brookes, A. Anders
REGISTRATION NUMBER: 36,373
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CORRENT APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US/OB
PILING DATE:
CIACOTTO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 4597 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity 59.58 tes 47; Conservative
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Best Local Similarity 65.19
Matches 41; Conservative
                                                                                                                                                                                                                                                     CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              linear
                     Rockville
                                        Maryland
                                                           USA
                                                                                 20850
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US-09-419-568F-25
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                                                           COUNTRY:
                     CITY:
STATE:
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CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                                                                                                                                                                        0;
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                                                                                                                                                                                                                                                                                                 DB 1; Length 5643;
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                                                                                                                                                                                                                                                                                                                                      27; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Corley, Neil C.
APPLICANT: Guegler, Karl J.
APPLICANT: Yue, Henry
TILLE OF INVENTION: HUMAN NUCLEIC ACID METHYLASES
NUMBER OF SEQUENCES: 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Chaganti, Raju S.K.
APPLICANT: Dyomin, Vadim
APPLICANT: Dalla-Favera, Riccardo
TITLE OF INVENTION: CLONING AND USES OF BCL-8
FILE REFERENCE: 53828-A-PCT-US
CURRENT APPLICATION WUMBER: US/09/450,852
CURRENT FILING DATE: 1999-11-29
NUMBER OF SEQ ID NOS: 4
SOFFWARE: Patentin Ver. 2.1
                                                                                                                                                                                                                                                                                               Score 27.8; DB Pred. No. 7.6; 0; Mismatches
                                         19603/10140
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Patent No. 6096526
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Hillman, Jennifer L. APPLICANT: Lal, preeti
NAME: TIMIAN, SUSAN J.
RECISTRATION NUMBER: 34,103
REFERENCE/DOCKET NUMBER: 196
TELECOMMUNICATION INFORMATION:
TELEPHONE: 716-263-1636
                                                                                                                                                                                                                                                                                               Query Match 27.5%;
Best Local Similarity 62.0%;
                                                                                                                                                    LENGTH: 5643 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                        TELEFAX: 716-263-1600
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                  44; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3831 AAAGTTTTCAA 3841
                                                                                                                                                                                                                  ; TOPOLOGY: linear; MOLECULE TYPE: CDNA
US-08-144-6028-4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; TYPE: DNA
; ORGANISM: human
US-09-450-852-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQ ID NO 3
LENGTH: 2340
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APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                    Matches
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1466 CITAATITTCATCCTGGGGGGATTTTTCTTCCTTGGCAAITCIIIIGIII | 1407
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 1894;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                22; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
                                                                                                                                                                                  Word Perfect_6.1 for Windows/MS-DOS 6.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Hillman, Jennifer L.
APPLICANT: Lal, Preeti
APPLICANT: Corley, Neil C.
APPLICANT: Corley, Neil C.
APPLICANT: Guegler, Karl J.
APPLICANT: Yue, Henry
IIILE OF INVENTION: HUMAN NUCLEIC ACID METHYLASES
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         26.5%; Score 26.8; I
64.5%; Pred. No. 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3: INCYTE PHARMACEUTICALS, INC
3174 PORTER DRIVE
INCYTE PHARMACEUTICALS, INC
                                                                                                                                                                                                                                                       CLASSIFICATION.
ATTORNEY/AGENT INFCMATION:
NAME: CERRONE, MICHEL C.
REGISTRATION NUMBER: 39,32
REFERENCE/DOCKET NUMBER: PF-0520 US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/575,205
                                                                                                                                                                                                                   US/09/082,310
                                                                                                                                                               PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 3, Application US/09575205
Patent No. 6436683
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                 TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 855-0555
TELEPAX: (650) 845-4166
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
                                                                                                                              E: Floppy disk
IBM PC compatible
               PALO ALTO
CALIFORNIA
                                                                                                                                                                                                                                                                                                                                                                                                                                          1894 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity 64.59
Matches 40; Conservative
                                                                                                                                                                                                CURRENT APPLICATION DATA:
APPLICATION NUMBER: US
                                                                                                                                                                                                                                  Herewith
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COMPUIER READABLE FORM:
                                                                                                         COMPUTER READABLE FORM:
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CLONE: 2124957
                                                                                                                                                                                                                                                                                                                                                                                                                                                             nucleic acid
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CALIFORNIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   linear
                                                                                                                                                               OPERATING SYSTEM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: nucleic
STRANDEDNESS:
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                                                                        USA
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                                                                                                                              MEDIUM TYPE:
                                                                                          94304
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                                                                                                                                                                                  SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SIATE: CA
                                                                                                                                                COMPUTER:
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                                                                       COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SIREET:
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                                                     SIATE:
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Application US/09302620B
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; ORGANISM: Candida tropicalis
US-09-302-6208-90
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REGISTRAIION NUMBER: 33,1
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AITORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity 69.2
hes 36; Conservative
                                                                                                                                                                                                                APPLICANT: Tang, Maria
APPLICANT: Loper, John C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Emeryville
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: 07
CLASSIFICATION:
                                          Patent No. 6331420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            20 CTGACTCATTAGAGCTGGAJGCCITTTCCTGTTGATAATTCTTTCTGTTTCATTA 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0: Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                 Ouery Match
25.5%: Score 26.8; DB 4; Length 1894;
Best Local Similarity 64.5%; Pred. No. 12;
Matches 40; Conservative 0; Mismatches 22; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2813 GTTGGCTTTTCTAATCTTGTTAAATATTTCTATTTTACCAAAGGTATTAA 2864
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: GOO, Zeren
APPLICANT: GOO, Zeren
APPLICANT: Hart, Charles E.
APPLICANT: Piddington, Christopher S.
APPLICANT: Sheepard, Paul O.
APPLICANT: Sheepard, Paul O.
APPLICANT: Gilbertson, Debra G.
APPLICANT: Gilbertson, Debra G.
APPLICANT: GROWTH FACIOR HOWOLOG ZVEGF3
FILE REFRENCE: 98-60
CURRENT APPLICATION NUMBER: US/09/457,066
CURRENT FILING DAIE: 1999-12-07
NUMBER OF SEQ ID NOS: 50
SOFTWARE FASTSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 26.4; DB Fred. No. 18; 0; Mismatches
                                                                                ALVANALIA CHOLIA ANTOCHARIA CON NAME: CERRONE, MICHAEL C. REGISTRATION NUMBER: 39,132
REFRENCE/DOCKET NUMBER: PF-0520 US
TELECHUNICATION INFORMATION:
TELECHUNE: (650) 845-055
INPORMATION FOR SED ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1894 base pairs
TERMOTH: 1894 base pairs
STRANDENESS: SINGLE
                PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/082,310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 42, Application US/09457066; Patent No. 6432673
                                                                        ATTORNEY / AGENT INFORMATION:
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69.28;
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Best Local Similarity 69.28
Matches 36; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: CDS
LOCATION: (1049)...(2085)
1S-09-457-066-42
                                                                                                                                                                                                                                                                                                                                             LIBRARY: BRSTNOT07
CLONE: 2124957
---09-575-205-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Mus musculus FEATURE:
                                                                                                                                                                                                                                                                                                           linear
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                       IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
                                                        FILING DATE:
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APPLICANT: Obeson, Martin
TITLE OF INVENTION: CYTOCHROME P450 MONOOXYGENASE AND NADPH CYTOCHROME P450
TITLE OF INVENTION: CYTOCHROME P450 MONOOXYGENASE AND NADPH CYTOCHROME P450
TITLE OF INVENTION: OXIDOREDUCIASE GENES AND PROTEINS RELAIED TO THE CAMEGA
TITLE OF INVENTION: RELAING THERETO
TITLE OF INVENTION: RELAING THERETO
TITLE OF INVENTION: RELAING THERETO
CURRENT APPLICATION NUMBER: US/09/302.620B
NUMBER OF SEQ ID NOS: 109
SOFTWARE: PALENTING DATE: 1999-04-30
SOFTWARE: PALENTIN OF: 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             26.1%; Score 26.4; DB 4; Length 3826;
69.2%; Pred. No. 19;
tive 0; Mismatches 16; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   25 TCATIAGAGCTGGATGCCTTTTCCTGTCTTGATAATTCTTTCTTCTTCA 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INCORMATION:
GENERAL INCORMATION:
APPLICANT: Covacci, Antonello
IIILE OF INVENTION: Helicobacter Pylori Cagi Region
NUMBER OF SEQUENCES: 46
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFIWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      JMBER: US/08/477,451
07-JUN-1995
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZIP: 94608-2916
COMPUTER READABLE FORM:
MEDIUM IYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
GENERAL INFORMATION:
APPLICANT: Wilson, C. Ron
APPLICANT: Craft, David L.
APPLICANT: Birich, Dubley
APPLICANT: Eshoo, Mark
APPLICANT: Madduri, Krishna M.
APPLICANT: Brenner, Alfred A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 13
US-08-477-451-9/c
| Sequence 9, Application US/08477451
| Patent No. 5928865
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: Chiron Corporation
STREET: 4560 Horton Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                33,113
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LENGIH: 5599 base pairs
TYPE: nucleic acid
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INFORMATION FOR SEQ ID NO:
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                                                                                                                                         Gaps
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                                                                                          Score 26.4; DB 2; Length 5599;
Pred. No. 20;
0; Mismatches 26; Indels 0
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                                                                                                                                                                                                                                                                                                                                                                          Sequence 13, Application US/08477451
Sequence 13, Application US/08477451
Sequence 10, 5928865
GENERAL INFORMATION:
TITLE OF INVENTION: Helicobacter Pylori Cagi Region NUMBER OF SEQUENCES: 46
NUMBER OF SEQUENCES: 46
NUMBER OF SEQUENCE ADDRESS:
ADDRESSEE: Chiron Corporation
STREET: 4560 Horton Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTEY: USA
ZIP: 94608-2916
COMPUTER REDABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERAING SYSTEM: PC-DOS/NS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DAIA:
APPLICATION NUMBER: US/08/477,451
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: McClung, Barbara G.
REGISTRATION NUMBER: 33,113
REFERENCE/DOCKET NUMBER: 0335.002
RELECOMMUNICATION INFORMATION:
TELEPHONE: 510-601-2708
              TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-477-451-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: 510-655-3542
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
                                                                                            26.1%; 61.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: DNA (genomic)
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                                                                                                              Best Local Similarity 61.89
Matches 42; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity 61.8 Matches 42; Conservative
  single
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                                                                                                                                                                                                                                                                        1100 CITIGATA 1093
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STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                15-08-477-451-13
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                                                                                              Query Match
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RESULT 15 US-08-477-451-25/c

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Db 4717 TCTCTCAAAGCGIIAGIGGCGAAITCTTITTCCTCTITTGTAAITTCTTIGTCATCAIGT 4658
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                                                                                                                                                                                                                                                                         COMPUTER READBLE FORM:

KEDIUM TYPE: Floppy disk
COMPUTER: IBM_PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PREDENT Release #1.0, Version #1.30
CURRENT APPLICATION DAIA:
APPLICATION NUMBER: US/08/477,451
FILING DAIE: 07-UNW-1995
CLASSIFICATION: 435
ATTORNEY AGENT INFORMATION:
NAME: MCCLUMS, Barbara G.
FEGISTRATION NUMBER: 33,113
FIFTERPATION NUMBER: 33,113
Sequence 25, Application US/08477451
Patent No. 5928855
GENERAL INFORMATION:
APPLICANT: Covacci, Antonello
TITLE OF INTENTION: Helicobacter Pylori Cagi Region
NUMBER OF SEQUENCES: 46
CORRESPONDENCE ADDRESS:
ADDRESSES: Chiron Corporation
STREET: 4560 Horton Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Search completed: December 8, 2002, 07:52:41 Job time : 33.3657 secs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IELECOMMUNICATION INFORMATION:
IELEPHONE: 510-601-2708
IELEFAX: 510-655-3542
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INFORMATION FOR SEQ ID NO: 25:
SECUENCE CHARACTERISTICS:
LENGTH: 19932 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE IYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SIRANDEDNESS: single
IOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4657 CTTTGATA 4650
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                                                                                                                                                                                                                                                      USA
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                                                                                                                                                                                                                         627 GAAGGAGGIGCCGGGGTAGGAAGIGGGCIGGGGAAAGGTIAIAAATCGCCCCCCGCCTCG 686
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               867 ACGGGCGCICAGGGCGGGGGGGGGGGGGGAACGAGGAGGAGGACTCTGGGGGCGG 926
 179 TGAGCGCGATGGGCAGGAGGAGGGCAAGGGCAAGAGGGCGCGGAG-AAAGACCCTGAAC 237
                                  23B CTGCCGGGGCCCGCGCTCCCGGGCCCGCGTCCCCACCCCCACGCGCGCCTCCCCA
                                                                                                                                                                                                                                                                                                         807 CGGGCGCCTGGCGGCGAGGATTACCCGGGGAAGTGGTTGTCICCTGGCTGGAGCCGCGAG
                                                                                              538 GGGCCACCCGCCCTCGTCGGCCCCCGCCCTCTCCGTAGCCGCAGGGAAGC-GAGCCTGG
                                                                                                                                                            567 GAGGAAGAAGAGGTAGGTGGGCAGGCGGATGAGGGGTGGGGGACCCCTTGACGTCACCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human; tumour suppressor gene; oncogene; antitumour; cytostatic; cancer; tumour; CpG dinucleotide; single-nucleotide polymorphism; cytosine methylation; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Tumour suppressor gene derived chemically modified sequence #73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Berlin K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAS46351 standard; DNA; 6316 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2000DE-1019058.
2000DE-1019173.
2000DE-1032529.
2000DE-1043826.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          927 GICTITGGCCGCGGG 941
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              717 GTCGTTGGCCGGGGG 731
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Piepenbrock C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (EPIG-) EPIGENOMICS AG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2001-602752/68
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06-APR-2000; 2
07-APR-2000; 3
30-JUN-2000; 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        31-SEP-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 3
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208 CCGGACTGCGCCTCAGTCCTCCGTGCCAAGAACACGTCGCGGAGGCGCGGGCCAGCTTCC 267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               328 CAGITICGGGCGCCCCCAGAGCTGAGTAAGCCGGGTGGAGGGAGTCTGCAAGGAITTCC 387
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TGAGCGCGATGGGCAGGAGGGGCAAGGGCAAGAGGCGCGGAGCAAAGACCCTGAAC 447
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  flt gene encoding receptor type tyrosine kinase. The promoter is useful for the tissue specific expression of heterologous proteins. Vectors contg. the DNA were used to transform vascular endothelial cells, such that a protein of interest could be expressed. The ligand controlling the function of the promoter may be used as a neovascularisation inhibitor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The DNA (nucleotides -229 to +8) contains a promoter for the human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Promoter of human flt gene encoding receptor ty\mu e tyrosine kinase useful for tissue specific expression of heterologous proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               tyrosine kinase receptor; ilt gene; promoter; neovascularisation;
tissue-specific expression; heterologous protein production; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         'n
                                                                                                                                                                                                                                                    Promoter of human flt gene encoding tyrosine kinase receptor.
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Pred. No. 9.5e-125;
0; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 840 BP; 120 A; 269 C; 336 G; 115 T; 0 other;
                                                               1400 ACGAGGACGACTCTGGCGGCCGGGTTTGGCCGCGGG 1440
                                              ACGAGAGGACTCTGGCGGCCGGGTCTTTGGCCGCGGG 941
                                                                                                                                                                                                                                                                                   receptor; flt gene;
                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
771..833
/*tag= a
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                                                                                                                                                        AAT08550 standard; DNA; 840 BP
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les 725; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          94JP-0084526
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                                                                                                                                                                                                                      (first entry)
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P-PSDB; AAR77646.
                                                                                                                                                                                                                                                                                 tyrosine kinase
                                                                                                                                                                                                                                                                                                                                                                                                                           JP07289263-A.
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                                                                                                                                                                                                                                                                                                                                  sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        22-AFR-1994;
                                                                                                                                                                                                                      18-JUN-1996
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                                                                                                                                                      The invention relates to a nucleic acid comprising a sequence of 18 bases, of a segment of chemically pretreated DNA (CP DNA) e.g. with bisulphite, of genes associated with tumour suppression and oncogenes having a sequence taken from 536 (actually 533 since numbers 408, 458 and 500 are missing from the sequence listing) sequences (Ss) and sequences complementary to (Ss). The nucleic acid may be a peptide nucleic acid-oligomer (PNA) of at least 9 nucleotides and may form part of a set of probes for detecting the cytosine methylation state and/or single nucleotide polymorphisms and also to be used in an array for analysing diseases associated with CpG dinucleotides e.g. ascertaining genetic and/or epigenetic parameters for the diagnosis and/or therapy of existing diseases or the predisposition to specific
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        compared to another set of genetic and/or epigenetic parameters, the differences serving as basis for diagnosis and/or prognosis events which are disadvantageous to patients. The present sequence is one of the
    modified genes associated with tumour suppressor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (ST*
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 241 ACCGTCGCGGAGGCGCGCCAGCTTCCCTTGGATCGGACTTTCCGCCCCTAGGGCCAGGC 300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             diseases, by analysing cytosine methylations. The parameters may be
                       genes and oncogenes, useful in designing primers and probes for analysing diseases associated with cytosine methylation state e.g.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              121 CTCCGGTGCCTTCCTAGACTTCTCGGGACAGTCTGAAGGGGTCAGGAGCGGCGGGACAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITCGGTGTTTTTTTAGATTTTCGGGATAGTTTGAAGGGGTTAGGAGCGGCGGGATAGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                533 genomic sequences derived from tumour suppressor genes and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    65.1%; Score 613; DB 22; Length 6316; llarity 78.2%; Pred. No. 6.4e-114; Conservative 0; Mismatches 205; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 of the printed specification, but was obtained in electronic format directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The sequence data for this patent did not form part
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 6316 BP; 1490 A; 255 C; 1803 G; 2768 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 itp.wipo.int/pub/published_pct_sequences.
                                                                                                                ID No 73; 27pp; English.
Fragments of chemically genes and oncogenes, use
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
es 736; Conserv
                                                                                                                SEQ
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                                                                                                                  Claim 1;
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Ine invention relates to a nucleic acid comprising a sequence of at least bases of a segment of chancelly pretreated bWh or games associated with cell signalling. The activity of the modified sequences of the invention may be described as cytostatio. The object of the invention is to provide the chancelly modified DNA of genes associated with cell signalling, as well as oligonucleotides and/or PNA-oligomers for particularly suitable for the diagnosis and/or therapy of genetic and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nucleic acid, useful for diagnosis and therapy of diseases associated with cell signalling e.g. cancer, comprises chemically modified genomic sequences of genes associated with cell signalling
                                                                                                                                                                                             5051
             4991
                                                                     780
                                                                                                              720
541 CCGIAGCCGCAGGGAAGCGAGCCIGGGAGGAGAAGAGGGGIAGGIGGGGAGCGGAIGAG 600
                                                                                                            661 AAGGITATAAATGGCCCCCCCCCCCCCGCTGCTCCATCGAGGTCCGCGGGAGGCTCGGA
                                                                                                                           GCGCCCAGGCGACACICCITCGGCTCCTCCCCCGGCAGCGGCGGCGGCGCTCGGAGCGGG
                                                                                                                                                                                    GGGIGGGGGACCCCTTCACGICACCAGAAGAGGGCCCCGGGGIACGAAGIGGGCIGGGGA
                                                                                                                                                                                                                       781 CICCGGGGCTCGGGTGCAGCGGCCAGCGGCGCCTGGCGGCGAGGATIACCCGGGGGAAGI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Cell signalling; cytosine methylation; cell signalling disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 1; SEQ ID NO 105; 24pp-sequence listing; English
                                                                                                                                                                                                                                                                                                                                                    5172 ACGAGAGGACGGATTTISGCGGTCGGTCGTTGGTCGCGGG 5212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Chemically treated cell signalling DNA sequence#53.
                                                                                                                                                                                                                                                                                                                                    ACGAGAGGACGGACTC/GGCGGCCGGGTCTTTGGCCGCGGG 541
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cytostatic; ds
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2000DE-1043826
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               cancer; tumour;
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01-SEP-2000;
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epigenetic parameters or genes associated with cell signalling. The chemically modified DNA provided by the invention is useful for diagnosis and thurspy of diseases such as solid tumours and cancer. The sequences given in records ABL70111-ABL70626 represent chemically pre-treated genomic DNA's of genes associated with cell signalling. Note: The sequence data for this patent is not represented in the printed specification, but is based on sequence information supplied by the
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                                                                                                                                              Sequence 6316 BP; 1490 A; 255 C; 1803 G; 2768 P; 0 other;
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                                                                                                                                                                             Maton 65.1%; Score 613; DB 24; Local Similarity 78.2%; Pred. No. 6.4e-114; es 36; Conservative 0; Mismatches 205;
                                                                                                                European Patent Office.
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Himman, Gene regulation-associated gene, severe combined immunodeficiency, cardiac damage; inflammatory response, hemospilia, werner syndrome; astimate, HDR syndrome; consolital heart defect; Saethfe-Choten syndrome; renal disease; Preeclampsia, cardiac allograft vascular disease; colorectal damos; Preeclampsia, cardiac allograft vascular disease; colorectal damos; Argord cancer, cesopiageal bancer; ds. tunour; himmunostimulant; cardiant, antihinflammatory; cosqulant; antiasthmatic; nephrotropic; gynecological; anti-tumour; immunosuppressive; cytostatic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to 224 nucleic acid sequences comprising at least is bases of a chemically pretreated gene associated with gene regulation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New nucleic acid sequences from chemically modified genes associated with gene regulation, useful for analysing cytosine methylations for diagnosis and therapy of diseases e.g. severe combined immunodeficiency
5112 GGIIGITITIIGGIIBBAGICGCGAGACGGGCGIIIAGGGCGBGGGICGGCGGGGGGGGA 5171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                and therapy of e.g. severe combined immunoueficiency disease, cardiac disorders, haemophilia, solid tumours and cancer, werner syndrome, astima, HDR syndrome, Saethre-Chotzen syndrome, renai disease,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      selected from 43 known genes (or complementary sequences). The Cremical pretreatment converts cytosine bases unmetnylated at the Greatment to uncorner bases with hybridistantic behaviour dissimilar to cytosine, to enable analysis of cytosine methylations. Inc DNA sequences, cliqomers (or sets/arrays) and method are useful in the diagnosis of diseases (or predisposition to diseases) sacciated with gene regulation and in therapy of such diseases, by enabling analysis or the cytosine methylation patterns of such genes, kits are provided. They are especially useful in diagnosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           preeclampsia, graft Persus-host disease. The present sequence is a sequence included in the sequence data for this specification and is associated with the numan gene regulation-associated genes.
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                                                                                                                                                                                                                                                                                                                  Human gene regulation-associated gene oligonuclectide #125
                                         901 ACCAGAGGACGGACTCTGGCGGCCGGGTCTTTGGCCGCGGG 541
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2000DE-1043826.
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30-JUN-2000;
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ABK31260 standard; DNA; 6316 BP

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Sequence 6316 BP; 1490 A; 255 C; 1803 G; 2768 T; 0 other;
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                                 Score 613; DB 24;
Pred. No. 6.4e-114;
                                   65.1%;
78.2%;
                                                                    Matches 736; Conservative
                                 Query Match
Best Local Similarity
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Human, signal transduction associated gene, cytosine methylation state, CpG island; signal transduction associated disease, solid tumour; cancer, antitumour; cytostatic, mutant; ds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   modified using a solution of bisulphite, hydrogen supplies or disulphite. Also disclosed are oligonucleotides and/or PNA oligoners for detecting the cytosine methylation state (CpG islands) of these genes, and a method for the dispinosis and/or therapy of genetic and epigenetic parameters of genes associated with signal transduction. The genemic by can be obtained from cells or cellular components which contain DNA, e.g. cell lines, biopsies, blood, sputum, scool, urine, cerebral spinal fluid, tissue embedded in parafilin such as tissue from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     sequences of the invention are useful for the diagnosis and therapy of diseases associated with signal transduction e.g. solid tumours and cancer. ABK31158-ABK31545 represent chemically pretreated genomic DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Note: The sequence data for this patent did not form part of the printe specification, but was obtained in electronic format directly from the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Oligonuclectide for diagnosis and therapy of diseases associated with signal transduction e.g. cancer, comprises chemically modified genomic sequences of genes associated with signal transduction –
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               eyes, intestine, kidney, brain, heart, prostate, lung, breast or liver, histologic object slides, and all their possible combinations. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4332 GIGHTAAGTAAGCGITAGTITITITITAGGCGITTTAGGTTTAGGTTTAGGTTTAGTGTTTGTGCGAGGGT 4391
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present invention relates to chemically modified DNA sequences of signal transduction associated genes. The DNA sequences are chemically
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 6316 BP; 1490 A; 255 C; 1803 G; 2768 I; 0 other;
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                                                                                                                        Signal transduction associated gene modified DNA #52.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 1; SEQ ID No 103; 24pp; English.
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01-SEP-2000; 2000DE-1043826.
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                                                                                (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (EPIG-) EPIGENOMICS AG
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les 736; Conserv
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                                                                                                                                                                                                                                                     AGCACCTCCCCACGCGCGCTCGGCCCCCGGCCACCCGCCCTCGTCGGCCCCCCGCCCTCT
                                                                                                                                                                                                                                                                                                                 601 GGGTGGGGGACCCCTTGACGTCACCAGAAGGAGGTGCCGGGGTAGGAAGTGGGCTGGGGA
                       181 GCGGGAAGAGCAGGCAAGGGGAGACAGCCGGACTGCGCCTCAGTCCTCCGTGCCAAAAC
                                                                    ACCGTCGCGGAGGCGCGGGCCTTCCCTTGGATCGGACTTTCCGCCCCTAGGGCCAGGC
                                                                                                                                                                                                                                                                                                  661 AAGGTTATAAATCGCCCCCCCCCCCCCCTCCTTCATCGAGGTCCGGGAGGCTCGGA
                                                                                                                                                                                                         AGAGGCCCCGGAGCAAAGACCCTGAACCTGCCGGGCCGCGCTCCCGGGCCCGCGTCGCC
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The invention relates to a nucleic acid (1) comprising a segment of 18 bases of chemically pretreated DNA of angiogenesis associated genes (11) related oligomers, (ABG66971-ABG67188) or their complements. (1), also related oligomers, are used to evaluate the methylation status and/or single-nucleotide polymorphisms, in angiogenesis-related genes, for neovascular glaucoma, solid tumours, inflammation, theumatoid arthritis, oligetto retinopathy, macular degeneration caused by reovascularisation, postatsis, arteriosclerosis, inflammatory bowel diseases, ulcers and cronn's disease.

anylogenesis-associated genes, useful for determining methylation status, e.g. in diagnosis or treatment of cancer

New nucleic acid fragments from chemically treated

WPI; 2002-500450/53.

Schacht O;

06-DEC-2001; 2001WO-EP14320 06-DEC-2000; 2000DE-1061338

W0200246454-A2 13-JUN-2002. (BPIG-) EPIGENOMICS AG.

Claim 1; SEQ ID NO 93; 41pp + Sequence Listing; German.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO

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                                                                                                                                                                                                      61 GIGCCAAGCAAGCGTCAGIICCCCICAGGCGCTCCAGGIICAGIGCCIIGIGCGGAGGGT 120
                                                                                                                                                                                                                                                                                                                                                                                                                      241 ACCGICGCGGAGGCGCGGCCAGCTICCCTIGGAICGGACTIICCGCCCCIAGGGCCAGGC 300
                                                                                                                                                                                                                                                                              121 CTCCGGTGCCTICCTAGACTICTCGGGACAGTCTGAAGGGGTCAGGAGGGGGGGGACAGC 180
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                                                                         Length 6321;
                               sequence 6321 BP; 1489 A; 258 C; 1805 G; 2769 I; 0 other;
                                                                                                          Indeis
                                                                    Score 613; DB 24; Dred. No. 6.4e-114; O; Mismatches 205;
at ftp.wipo.int/pub/published_pct_sequences.
                                                                     65.18;
78.28;
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inflammation; rheumatoid arthritis; diabetic retinopathy; antiulcerds; macular degeneration; inflammatory bowel disease: Crohn's disease; antirheumatic; antidiabetic; antipsoriatic;

antiarteriosclerotic; ds

Homo sapiens

Human anglogenesis associated polynucleotide SEQ ID NO 93.
Human; anglogenesis; methylation; eye disease; glaucoma; tumour;

ABQ67063 standard; DNA; 6321 BP

ABQ67063

(first entry)

28-AUG-2002

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Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Fragments of chemically modified genes associated with tumour suppressor genes and oncogenes, useful in designing primers and probes for analysing diseases associated with cytosine methylation state e.g.
                                                                          4931
                                                                                                                                                                                                                                                                                                                                                            Human, tumour suppressor gene; oncogene; antitumour; cytostatic; cancer; tumour; CpG dinucleotide; single-nucleotide;polymorphism; SNP;
                                                                                                                                     840
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                                                                                                                                                                                              GGTTGTCTCCTGGCTGGAGCCGCGAGACGGGCGCTCAGGGCCCGGGGGCCGGCGGCGGCGGCGA 900
                                   GGGTGGGGGACCCCTTGACGTCACAGAAGGAGGTGCCGGGGTAGGAAGTGGGCTAGGGG
                                                                  781 CICCGGGGCTCGGGTGCAGCGGCCAGCGGCGCCTGGCGGCGAGGATTACCCGGGGAAGT
                         541 CCGTAGCCGCAGGGAAGCGAGCCTGGGAAGAAGAAGAGGGTAG3FGGGGAGGCGATGAG
                                                                                          GOGGGCCAGGCGGACACTCCTCGGCTCCTCCCCGGCAGCGGCGGCGGCTCGGAGCGGG
                                                                                                                                                                                                                                                                                                                                           Tumour suppressor gene derived chemically modified sequence #74.
                                                                                                                                                                                                                                       ACGAGAGGACGGACTCTGGCGGCGGGGTCTTTGGCCGCGGG 541
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 1; SEQ ID No 74; 27pp; English
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AAS46352/c
ID AAS46352 standard; DNA; 6316
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2000DE-1019173.
2000DE-1032529.
2000DE-1043826.
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                                                                                                                                                                                                                                                                                                                                                                           cytosine methylation; ds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (EPIG-) EPIGENOMICS AG
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The invention relates to a nucleic acid comprising a sequence of 18 bases, of a segment of chemically pretreated DAM (CP DAM) e.g. with bisulphite, of genes associated with tumour suppression and oncogenes having a sequence taken from 536 (actually 533 since numbers 408, 458 and 500 are missing from the sequence listing) sequences (SS) and sequences complementary to (SS). The nucleic acid may be a peptide nucleic acid-oligomer (PNA) of at least 9 nucleotides and may form part of a set of probes for detecting the cytosine methylation state and/or single nucleotide polymorphisms and also to be used in an array for analysing diseases associated with CpC dinucleotides e.g. cancers and tumours. The probes can also be used in an exthod for secretaining genetic and/or epigenetic parameters for the diagnosis and/or therapy of existing diseases or the predisposition to specific
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 533 genomic sequences derived from tumour suppressor genes and oncogenes. Sequences with even numbered Seq ID numbers are the complementary sequence of the corresponding odd numbered sequence (e.g. ID 2 and ID1, ID 536 and ID 535, except for those whose partner sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Which
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         diseases, by analysing cytosine methylations. The parameters may be compared to another set of genetic and/or epigenetic parameters, the differences serving as basis for diagnosis and/or prognosis events were diseavantageous to patients. The present sequence is one of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              62 IGCCAAGCAAGCGICAGIICCCCICAGGCGCTCCAGGIICAGIGCCIIGIGCCGAGGGIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TCCGGTGCCTTCCTAGACTTCTCGGGACAGTCTGAAGGGGTCAGGAGGGGGGGACAGCG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pot_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 6316 BP; 1474 A; 255 C; 1549 G; 3038 T; 0 other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             is missing). Note: The sequence data for this patent did not form
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         54.3%; Score 510.8; DB 22; 71.5%; Pred. No. 1.8e-93; ive 0; Mismatches 267;
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Matches 671; Conservative
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The invention relates to a nucleic acid comprising a sequence of at least 18 bases of a segment of chemically pretreated DNA of genes associated with cell signalling. The activity of the modified sequences of the invention may be described as cytostatic. The object of the invention is signalling, as well as a cytostatic. The object of the invention is signalling, as well as a lighten object of a method which is particularly suitable for the diagnosis and/or therapy of genetic and epigenetic parameters of genes associated with cell signalling. The chemically modified DNA provided by the invention is useful for diagnosis and therapy of diseases such as solid tumours and cancer. The sequences given in records ABL70111-ABL70626 represent chemically pre-treated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  with cell signalling e.g. cancer, comprises chemically modified genomic sequences of genes associated with cell signalling
                                                                                                            1325
                                                                                                                                                                                                                                                                                                               1264 TCCGAAACTCGAATACAACGACCAACGAACGCTAACGAGGAAAATTAGGGGAAAAAIA 1255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nucleic acid, useful for diagnosis and therapy of diseases associated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Chemically treated cell signalling DNA sequence complementary to#53
                     TCCGGGGCTCGGGTGCAGCGGCCAGCGGCGCCTGGCGGCGAGGATTACCCGGGGAAGTG
                                                                                                                                                                                                                                                                                            842 GTTGTCTCCTGGCTGGAGCCGGGAGAGGGGGCTCAGGGCGGGGCCGGGGCCGGCGGCGGAA
602 GGTGGGGGACCCCTTGACGTCACCAGAAGGAGTGCCGGGGTAGGAAGTGGGCTGGGGAA
                                                                         662 AGGTTATAAATCGCCCCCCGCCCTCGGCTGCTCTTCATCGAGGTCCGCGGAGGCTCGGGG
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01-SEP-2000; 2000DE-1043826.
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            Note: The sequence data for this patent is not represented in the printed specification, but is based on sequence information supplied by the
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                                                                 Sequence 6316 BP; 1474 A; 255 C; 1549 G; 3038 T; 6 ciner;
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genomic DNA's of genes associated with cell signailing
                                                                                        Score 510.8; DB 24;
Pred. No. 1.8e-93;
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71.5%;
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Mismatches 267; Indels

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Matches 671; Conservative

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Human; Gene regulation-associated gene; severe combined immunodeficiency; cardiac damage; inflammatory response; ideamobilita; Werrer syndrome; casthma; HDR syndrome; congenital heart defect; Saethre-Chotzen syndrome; renal disease; Preeclampsia; cardiac allograft vascular disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                          colorectal cancer; thyroid cancer; oesophageal cancer; ds; tumour; immunostimulant; cardiant; antiinflammatory; coagulant; antiasthmatic; nephrotropic; gynecological; anti-tumour; immunosuppressive; cytostatic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New nucleic acid sequences from chemically modified genes associated with gene regulation, useful for analysing cytosine methylations for diagnosis and therapy of diseases e.g. severe combined immunodeficiency
                                                                                                                                                                                                                                                  Human gene regulation-associated gene oligonucleotide #126,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 1; SEQ ID No 130; 26pp; English.
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ID AAS61171 standard; DNA; 6316
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The invention relates to 224 nucleic acid sequences comprising at least 18 bases of a chemically pretreated gene associated with gene regulation selected from 43 known genes (or complementary sequences). The chemical pretreatment converts cytosine bases unmethylated at the 5-position to uracil or another base with hybridisation behaviour dissimilar to cytosine, to enable analysis of cytosine methylations. The DNA sequences, oligomers (or sers/arrays) and method are useful in the diagnosis of diseases (or predisposition to diseases) associated with gene regulation and in therapy of such diseases, by this are provided. They are especially useful in diagnosis of additional methylation patterns of such genes, kits are provided. They are especially useful in diagnosis and therapy of e.g. severe combined immunodeficiency disease, cardiac disorders, haemophilia, solid tumours and cancer, Werner syndrome, asthma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          preeclampsia, graft versus-host disease. The present sequence is a sequence included in the sequence data for this specification and is
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    associated with the human gene regulation-associated genes. Note: The sequence data for this patent did not form part
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ABK31261 standard; DNA; 6316

ABK31261;

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DB 24; Length 6316;

Score 510.8; DB 24 Pred. No. 1.8e-93;

54.3%;

Best Local Similarity

Query Match

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Sequence 6316 BP; 1474 A; 255 C; 1549 G; 3038 T; 0 other;

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                                                                                                            inflammation, rheumatoid arthritis, diabetic retinopathy, antiulcerds, macular degeneration; inflammatory bowel disease; Crohn's disease; antirheumatic, antidiabetic; antipsoriatic;
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                                                                                                                                  Human, signal transduction associated gene, cytosine methylation state, CpG island; signal transduction associated disease; solid tumour; cancer; antitumour; cytostatic; mutant; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       their complementary sequences.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from the Buropean Patent Office.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 signal transduction associated genes. The DNA sequences are chemically modified using a solution of bisulphite, hydrogen sulphite or disulphite. Also disclosed are oligonuclacideds and/or PNA oligoners for detecting the cytosine methylation state (cpc islands) of these genes, and a method for the diagnosis and/or therapy of genetic and epigenetic parameters of genes associated with signal transduction. The genomic DNA can be obtained from cells or cellular components which contain DNA, e.g. cell lines, biopsies, blood, sputum, stool, urine, cerebral-spinal fluid, tissue embedded in paraffin such as tissue from pistologic object slides, and all their possible combinations. The sequences of the invention are useful for the diagnosis and therapy of diseases associated with signal transduction e.g. solid tumograps and contains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Oligonucleotide for diagnosis and therapy of diseases associated with signal transduction e.g. cancer, comprises chemically modified genemic sequences of genes associated with signal transduction
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1924 TCCGATACCTTCCTAAACTTCTCGAAACAATCTAAAAAATCAAAAAGGACGAACAACG 1855
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2044 CCGAARAAAACACGAACACCCCCTAAAACCTAAACTAATTCGCAATCTICCCAAAAA 1985
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      62 TGCCAAGCAAGCGTCAGTTCCCCTCAGGCGCTCCAGGTTCAGTGCCTTGTGCCGAGGGTC 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    122 TCCGGTGCCTTCCTAGACTTCTCGGGACAGTCTGAAGGGGTCAGGAAGGGGAGCGGGACAGCG 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present invention relates to chemically modified DNA sequences of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 pretreated genomic DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cancer. ABK31159-ABK31545 represent chemically pretreated genomic DNN sequences of different genes associated with signal transduction, or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 CCGAAAAAAGACACGGACACGCTCCCCTGGGACCTGAGCTGGTTCGCAGTCTTCCCAAAGG 61
                                                                 Signal transduction associated gene modified complementary DNA #52.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .,
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0; Mismatches 267;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   29-JUN-2001; 2001WO-EP07472.
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2000DE-1043826.
   (first entry)
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671; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (EPIG-) EPIGENOMICS AG
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01-SEP-2000;
23-APR-2002
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                                                                                                                                                                                                                                                                                                            Synthetic.
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08: AAW44841.
                                                      602 GUIGGGGGAC
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AAV19347
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                                                                                                                                                                                                                                                                                                                                                          single-nucleotide polymorphisms, in angiogenesis related genes, for diagnosis and treatment of eye diseases, proliferature retinopathy. neovascular glaucoma, solid tumours, inflammation, rheumatoid arthritis, diabetic retinopathy, maqular degeneration caused by neovascularisation,
                                                                                                                                                                                                                                                                                    The invention relates to a nucleic acid (I) comprising a segment of 15 abases of chemically pretracted DNA of angiogenesis-associated genes (II) having sequences (AbQ6671-AbQ61178) or their complements (I), also related oligomers, are used to evaluate the methylation status and/or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1690
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                                                                                                                                                                                                                                                                                                                                                                                                                            psoriasis, arteriosclerosis, inflammatory bowel diseases, ulcers and Crohn's disease.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   242 CCGTCGCGGAGGCGGCCAGCTTCCCTTGGATCGGACTTTCCGCCCCTAGGGCCAGGCG
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                                                                                                                                                                             New nucleic acid fragments from chemically treated angiogenesis-associated genes, useful for determining methylation status, e.g. in diagnosis or treatment of cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     54.3%; Score 510.8; DB 24; Length 6321; 71.5%; Pred. No. 1.8e-93; Ive 0; Mismatches 267; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 6321 BP; 1474 A; 258 C; 1553 G; 3036 T; 0 other;
                                                                                                                                                                                                                                                      Claim 1; SEQ ID NO 94; 41pp + Sequence Listing; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ftp.wipo.int/pub/published_pct_sequences.
                                   2000DE-1061338
06-DEC-2001; 2001WO-EP14320
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Matches 671; Conservative
                                                                       (EPIG-) EPIGENOMICS AG.
                                                                                                                                             WPI; 2002-500450/53.
                                   06-DEC-2000;
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1269 INCORARCIC:RAIRCRACGACCARCGARGCCIRACGAGARAITACCCGARARARIA 1210
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This cLNA clone codes for human soluble FLT-1 (sFLT-1, see AAW44841), the tyrosine klasse receptor (TKR) for human vascular endothelial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Inhibition of anglogenesis, particularly in tumours - by using DNA expressing a scluble form of a tyrosine kinase receptor which forms a dimer with a ascular endothelial growth factor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FLI-1; SFLI-1; vascular endothelial growth factor; VEGF, sVEGF-RI, receptor tyrosine kinase; signal transduction; angiogenesis; gene therapy; timour; metastasis; inflammation; psoriasis; rheumatoid arthibis; haemangioma; diabetic retinopathy;
                                                                                                                        ABBITATAAA BOGCCCCCCCCCCCTCGCTCTTCTTCCATCGAGGTCCGGGGAGGCTCGGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                             782 iccoggeresserseadecaceaeceaecereeceaeceaecarraceeceaeaagre
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                                                                                                                                                                                                                                                                                                                           722 CECECCAGGC BACACTCCTCTCGGCTCCTCCCCGGCAGCGGCGGCGGCGCCTCGGAGCGGGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              angiofibroma; mecular degeneration; human; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human soluble VESF receptor FLT-1 cDNA.
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250..2313
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             850 CTGGCTGGAGCCGCGAGACGGCGCTCAGGGCGCGGGGCCGGCGGCGGCGAACGAGGGA 909
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    119 CTGGCTGGAGCCGCGAGACGGGCGCTCAGGGCGCGGGGCGGGGGAACGAGAGA 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           receptor protein which binds to VEGF in extracellular regions adjacent to the primary tumor and vascular endothelial cells. Formation of a SVEGF-R/VEGF complex prevents binding of VEGF-#6 the FLT-I TRR, antagonising transduction of the normal intracellular signals associated with vascular endothelial cell-induced tumour angiogenesis. Expression of a soluble TRR may also impart a therapeutic effect by binding either with or without VEGFs to form
                                                                                                                                                                                                                                                                                                                                      non-functional heterodimers with full-length VEGF-specific TKRs and thereby inhibiting the mitogenic and anglogenic activities of
                                                                        psoriasis, rheumatoid arthritis, haemangioma, diabetic retinopathy, angiofibroma and macular degeneration. For primary tumour growth and metastasis, this involves traffer of a nucleotide sequence encoding a soluble form of VEGF TRE on amamalian (human) host, preferably using an adenovirus or recombinant plasmid DNA vector. The transferred nucleotide sequence transcribes mRNA and a soluble
growth factor (VEGF). PCR cloning was used to obtain the fit-1 derived TRR (SVEGR-RI) stitl-1 cDNA from a HUVEC CDNA library. The invention relates to methods of gene therapy for inhibiting angiogenesis associated with solid tumor growth, tumour metastasis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Vascular endothelial cell growth factor; VEGF; receptor; inhibitor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              soluble; treatment; angiogenesis; psoriasis; tumour; arthritis; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 19; Length 2313;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    receptor/inhibitor (SVEGF-RI) encoding cDNA.
                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 2313 BP; 705 A; 537 C; 539 G; 532 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /product= " soluble VEGF inhibitor'
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 194.8; DB 1
Pred. No. 3.2e-30;
0; Mismatches 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          910 CGGACTCTGGCGGCCGGGTCTTTGGCCGCGGG 941
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250..2313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAV09330 standard; cDNA; 2313 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         20.7%;
98.1%;
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93US-0038769.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity 98.1 Matches 208; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        21-APR-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             21-APR-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              25-MAR-1993;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           Watch Match
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                                                                                                                                                                                                                                                                                                                                        specifically VEGF-induced angiogenesis, particularly for treatment of psorliasis, 'Itematofia arthritis, hemandylomas, angiofibromas, diabetic retinopathy, neovascular glaucoma or tumour vascularisation. The sVBGF-RI can be administered topically or intravenously or from slow-release
                                                                                                                                                                                                                                                                                                   fragment of the VEGF receptor that binds VEGF with high affinity but is unable to transduce a signal, sVEGF-RI is used to inhibit VEGF activity, specifically VEGF-induced angiogenesis, particularly for treatment of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VEGF; human; primer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  730 GCGGACACICCICTCGGCTCCTCCCCGGCAGCGGCGGCGGCICGGAGCGGCCTCCGGGGC 789
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 ICGGGTGCAGCGGCCAGCGG--GCCTGGCGGGGGAGATAACCCGGGGAAGTGGTTGTCC 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 GCGGACACICCTCTCGCCTCCTCCCCGCCACCGCGCGCGCTCCGAACGCGCTCCGGGGC 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       amplification; PCR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /product- "VEGF receptor extracellular domain" /note= "no stop codon is given at the 3' end of the
                                                                                                                                                                                                                                                                   cDNA encodes a soluble inhibitor of vascular endothelial cell or (VEGF). The VEGF receptor/inhibitor (SVEGF-RI) represents a
                                                                                                                                          growth factor receptor - and related vector and transformed cells, expressing scluble inhibitor of VEGF useful for inhibiting
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         790 TCGGGTGCAGCGGCCAGCGGCGCCTGGCGGCGAGGATTACCCGGGGAAGTGGTTGTCTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              angiogenesis: e.g. for treatment of psoriasis, arthritis, tumours
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 19; Length 2313;
                                                                                                                       Nucleic acid encoding soluble form of vascular endothelial cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human VEGF receptor extracellular domain coding sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 2313 BP; 705 A; 537 C; 539 G; 532 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Immunoglobulin-like domain; extracellular domain; vascular endothelial cell growth factor receptor; truncation; mutant; tumour; vascularisation; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 194.8; DB 1
Pred. No. 3.2e-30;
0; Mismatches 2
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                                                                                                                                                                                                                                Claim 3; Fig 2A-B; 47pp; English.
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idenity 98.1%;
Conservative 0
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316..2523
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                                 Thomas KA;
(MERI ) MERCK & CO INC
                                                                   WPI; 1998-120332/11.
P-PSDB; AAW47036.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
                                                                                                                                                                                                                                                                                      factor (VEGF
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                                 Kendall RL,
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This is the nucleotide sequence encoding the lst-7th immunoglobulin-like domains of the extracellular domain of VECF (vascular endothelial cell growth factor) receptor FLT. The sequence is amplified by the primars ANV01458-V01459. The VECF receptor sequence can be used to generate truncated mutants which comprise the immunoglobulin-like domains 1-3, 1-4, 1-5 or 1-7. The polypeptides can be used in treatment of solid tumours and other diseases accompanied by pathological vascularisation since they inhibit vascularisation by stimulation with VECF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     850 CIGGCIGGAGCCGCGAGACGGGCGCTCAGGGCCGGGGCCGGCGGCGGCGAACGAGGA 909
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2; Gaps
                                                                                                                                                                                                                                       Vascular endothelial growth factor binding polypeptide(s) - used in the treatment of solid tumours etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 194.8; DB 18; Length 2523;
Pred. No. 3.2e-30;
0; Mismatches 2; Indels 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 2523 BP; 765 A; 596 C; 589 G; 573 T; 0 other;
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                                                                                                                                                                                                                                                                                 Disclosure; Page 9-12; 19pp; Japanese.
                                                                                                                                                            (TOAG ) TOA GOSEI CHEM IND LTD.
                                                                                                                             96JP-0066711.
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Best Local Similarity 98.1%;
Matches 208; Conservative
                                                                                             96JP-0066711
   /*tag= c
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P-PSDB; AAW36138.
                               JP09255700-A
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 1444 AATAAAAACCCCTTAACGTCACCAAAAAAAATACCGAAATAAAAATAAAATTAAACTAAAAA 1385
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="synthetic construct"
/db_xref="taxon:32630"
/note="chemically treated genomic DNA (Homo sapiens)"
a 255 c 1549 g 3038 t
                                                                                                                                                                            782 ICCGGGGCICGGGIGCAGCGGCCAGCGGCGCCTGGCGGCGAGGATIACCCGGGGAAGIG 841
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                                     AGGITATAAATCGCCCCCCCCCCCCCCTCGCTCTTCATCGAGGTCCGCGGGAGGCTCGGAG
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54.3%; Score 510.8; DB 6; Length 6316;
Best Local Similarity 71.5%; Pred. No. 6.8e-74;
Matches 671; Conservative 0; Mismatches 267; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Olek, A., Piepenbrock, C. and Berlin, K. Diagnosis of diseases associated with the cell cycle Patent: WO 0168911-A 130 20-SEP-2001;
                                                                                                                                                                                                                                                                                                                                          1144 CGAAAAACGAACTCTAACGACGAATCGTTAACCGCG 1107
                                                                                                                                                                                                                                                                                                                         CGAGAGGACGGACTCTGGCGGCCGGGTCTTTGGCCGCG 939
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TITLE
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Diagnosis of diseases associated with tumor suppressor genes and
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                                                                                                                                                                                                                                                                                                                                                                        /organism="synthetic construct"
/db_xref=ctaxon:32550*
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5172 ACCAGAGGACTTTTGGCGGTCGGGTCGTTGGTCGCGGG 5212
                                                                                      DNA
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Epigenomics AG (DE)
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Olek,A., Piepenbrock,C. a
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                  782 ICCGGGGCTCGGGTGCAGCGGCCAGCGGCGCCTGGCGGCGAGGATTACCCGGGGAAGTG
                                           GAGGGGGGGAGCAAAGACCCIGAACCIGCGGGGCGGCGCCTCCCGGGCCCGCGTCGCCA
                                                                                482 GCACCICCCCACGCGCGCTCGGCCCCGGGCCACCCGCCCTCGICGGCCCCCGGGCCCTCTC
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Diagnosis of diseases associated with cell signalling Patent: WO 0202807-A 106 10-JAN-2002: Epigenomics AG (DE)
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144096 bp DNA linear HIG 19-JUL-2002
Rattus norregious clone CH230-448N2, *** SEQUENCING IN PROGRESS
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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                    1269 TCCGAAACTCGAAIACAACGACCAACGAACGCCIAACGACGAAAAIIACCCGAAAAAIA 1210
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NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).
NOTE: This is a 'working draft' sequence. It currently consists of 57 conligs. The true order of the pieces is not known and their order in this sequence record is
Sutton, A., Svatek, A., Tabor, P., Tamerisa, A., Tamerisa, K., Tang, H., Tansey, J., Taylor, C., Taylor, T., Telfrod, B., Thomas, N., Thomas, S., Osmani, K., Vasquez, L., Vera, V., Villalon, D., Visson, R., Wang, A., Wang, A., Wang, S., Warnen, R., Washington, C., Wallington, S., Williams, G., Williams, G., Williams, G., Williams, G., Wulliamson, A., Wleczyk, R., Wooden, S., Worley, K., Wu, Y., Wu, Y., Wu, Y., Zorrilla, S., Nelson, D., Pirect Submission
Unpublished
                                                                                                                                                                                                                                                                    Worley, K.C.
Direct Submission
Submitted (19-JUL-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, IX 77030, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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Consensus quality: 10111 bases at least Q40
Consensus quality: 106747 bases at least Q30
Consensus quality: 110016 bases at least Q20
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123336: gap of unknown length
127745: contig of 4209 bp in length
137745: gap of unknown length
133861: contig of 5716 bp in length
133451: gap of unknown length
140523: contig of 7062 bp in length
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Search completed: December 8, 2002, 11:46:32 Job time : 2551.64 secs

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Database

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AU136034 AU136034 PLACEL Homo sapiens cDNA clone PLACE1003403 5', mRNA
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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HRI human cDNA project; 5'- & 3'-end one pass sequencing: Helix
Research Institute: CDNA library construction: Department of
Virology, Institute of Medical Science, University of Tokyo, and
Helix Research Institute.
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Tel: 81-438-52-3975
Fax: 81-438-52-3986
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Genomics Laboratory
Helix Research Institute
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Site_2: EcoRV (destroyed); RNA source anonymous pool of 6
male brains, age range 23-27 yo. Library is oligo-dI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens
Eukaryota: Metazoa: Chordata: Craniata: Vertebrata: Euteleostomi:
Mammalia: Eutheria: Primates: Catarrhini: Hominidae: Homo.

1 (bases 1 to 775) . -:- -...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: ILAM11480 row: n column: 23
High quality Sequence stop: 775.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           181 AGGCGGGGGCGGCGGCGGCGGCGACGACGACGACTCTGGCGGCCGGGTGGCC 240
                                                                                                                                                                                                                                                                                                                                                                                                                    877 AGGGCGCGGGCCGGCGCGCGCGACGACGACGACTCTGGCGGCCGGGTCTTTGGCC 936
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National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                             1 ATGGAGGTCCGCGGGGAGCTCGGAGCGCGCCAGGCGGACACTCCTCGGCTCCTCCCCG 60
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                                                                                                                                        7 others
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                                                                                                                                                                                           Score 243.4; DB 9
Pred. No. 4.7e-37;
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                                                                                                                                                                                                                          0; Mismatches
                                                                                                                        r: pME18SFL3"
220 g 126
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/db_xref="taxon:9606"
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                                                                 /clone_"PLACE1003403"
/clone_lib="PLACE1"
/tissue_type="placenta"
/note="Vector: pME18SFL
Location/Qualifiers
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BIB20974 906 bp mRNA linear EST 04-OCT-2001
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pCMY-SPORIG; Site_1: Noll, Site_2: ECOVY (destroyed): RNA
source anonymous pool of 6 male brains, age range 23.27: ]
male lung, age 27; and 1 male testis, age 69. Library is
primed and directionally cloned (EcoRV site is destroye upon clouding). Average insert size 1.5 Kb, insert size range 1-3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 019. Not this is a NIH MGC Library."
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Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostori;
Mammalia: Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 906)
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National Institutes of Health, Mammalian Gene Collection (MGC)
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                                                                                                                                                                                                                                                                                                                                                                                                               Email: cgapbe-remail.nih.gov
Tissue Procurement: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can
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Plate: LLAM11440 row: a column: 08
                                                                                                                                                                                                                                                             Score 232.4; DB 1
Pred. No. 5.9e-35;
0; Mismatches 1
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/db_xref="taxon:9606"
/clone="IMAGE:5176591"
/clone_lib="NHH_MGC_115"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         High quality sequence start: 2
High quality sequence stop: 765.
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B1820974
B1820974.1 GI:15932524
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BASE COUNT ORIGIN

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Length 1171;

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cDNA was primed with a NotI-coligo(dT) primer. Five prime end enriched, double-stranded cDNA was digested with Not I and cloned into the Not I and ECO RV sites of the pCMVSPORT 6 vector. Library was constructed by Life Technologies. Contact: Feng Liang Life Technologies, a division of Invitrogen 9800 Medical Center Drive Rockville. Maryland 20850, USA Fax: (1) 301 610 8371 Email: fliangelifetech.com URL. http://fulllength.linvitrogen.com"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AL541018
AL541018 LII_FL002_PL1 Homo sapiens cDNA clone CS0DE005Y102 5 prime AL541018
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Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
I (bases 1 to 826)
Livw. B., Gruber.C., Jessee,J. and Polayes,D.
Full-legth CDNA libraries and normalization
Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="Organ: placenta; Vector: pCMVSPORT 6; 1st strand
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                                                                                                                                                                                                                                                                                                               61 GGCTCGGAGCGGCTCCGGGGCTCGGGTGCAGCGGCCAGCGGGCGCCTGGCGGGGGGAT 120
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BP 191 91005 EVRI cedex - France
Email: segref@genoscope.cns.fr, Web : www.genoscope.cns.fr.
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                                                                                Score 230.8; DB 11; Deuy...
Pred. No. 1.2e-34;
     /note="Vector: pCMV-SPORT6"
340 a 260 c 302 g 269 t
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/lab_host="DH108"
                                                                                                                                               0; Mismatches
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/db_xref="taxon:9606"
/clone="CSODE005Y102"
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                                                                                                 24.5%;
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Best Local Similarity 99.6%
Matches 225; Conservative
                                                                                                                                            Matches 232; Conservative
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ALS47018
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Manmalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1171)
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Contact: amgfbcm.tmc.edu
Gunaratne, P.H., Garcia, A.M., Lu, X., Huljk, S.W., Hale, S.M.,
Yoon, V.S., Kowis, C.R., Lawrence, S., Marrin, R.G., Muzny, D.M.
Richards, S., Gibbs, R.A.
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/clone="IMAGE:51565g"
/tlssue_type="Brain, Lung, Testis. adult. pooled whole"
/clone_llb="NIH_MGC_lls"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gene Collection (MGC), Cancer Genomics Office, National Cancer -
Institute, 31 Center Drive, Room 11A03, Belhesda, MD 20892-2590,
Gruber (Invitrogen). Research Genetics tracking code 021. Note: this is a NIH_MGC Library." 228~c~264~g~194~t~l~others
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Email: cgapbs-rémail.nih.gov
Tissue Procurement: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)
DNA Sequencing by: Baylor Collège of Medicine Human Genome
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                                                                                                                   Score 230.8; DB 13; Length 906;
Pred. No. 1.2e-34;
0; Mismatches 2; Indels 0;
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BC029849
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Center code: BCM-HGSC
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24.5%;
Best Local Similarity 99.1%;
Matches 232; Conservative
            021. NO.
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LOCUS

RESULT 4 BC029849

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ACCESSION VERSION

KEYWORDS

SOURCE

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REMARK COMMENT

AUTHORS REFERENCE

0; Gaps

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FEATURES

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Sequence 1, Appli
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1 TATATCACAGATGIGCCAAA.......CGACAGCAGCACTCIGTIGG 2101
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/cgn2_6/ptodata/1/ina/5B_COMB.seq:*
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GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.
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US-08-193-8293-1
US-07-977-813-593-3
US-07-946-507-3
US-08-252-517-5
US-08-601-891-5
US-09-021-324-5
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US-08-901-710-1
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Maximum Match 1008
Listing first 45 summaries
                                                                                   - nucleic search, using sw model
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Gapop 10.0 , Gapext 1.0
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Maximum DB seq length: 2000000000
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Match Length DB
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              Sequence 3, A
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IIILE OF INVENTION: HUMAN RECEPTOR TYROSINE KINASE, KDR
WIMBER OF SEQUENCES: 8

CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: INP PC compatible
OPPRATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                    US-08-446-648-45
US-08-325-328-45
US-08-327-353-1
US-08-78-14-5
US-08-78-14-15
US-08-78-14-15
US-08-78-14-15
US-08-78-14-17
US-08-322-616-17
US-08-323-618-17
US-08-330-6918-21
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/098,707A
FILLING DATE: 17-Jun-1998
CLASSIFICATION: <U0Known>
                                                                                                                                                                                                      JS-08-183-211-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REGISTRATION NUMBER: 36,545
REFERENCE/DOCKE NUMBER: 19963PV
IELECOMUNICATION INFORMATION:
TELEPHONE: 732/594-3905
                                                                                                                                                                                                                                                         ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear
MOLECULE TYPE: CDNA
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: Merck & Co., Inc. SIREET: P.O. Box 2000
                                                                                                                                                                                                                                                                                                                  Sequence 1, Application US/09098707A
Patent No. 5204011
GENERAL INFORMATION:
APPLICANT: Kendall, Richard L.
                                                                                                                                                                                                                                                                                                                                                                        Ihomas, Kenneth A.
Mao, Xianzhi
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IYPE: nucleic acid
STRANDEDNESS: double
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NAME: Hand, J. Mark
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
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Matches 1077; Conservative
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                      US-09-098-707A-1
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                                             2126 AAGACTCAGGCAITGIAIIGAAGGAIGGGAACCGGAACCTCACTAICCGCAGAGIGAGGA 2185
1886 TIAAGAAIGCAICCIIGCAGGACCAAGGAGACIAIGICIGCCIIGCICAAGACAGSAAGA 1945
                                                                                                                2006 TCACAGGAAACCIGGAGAATCAGAGGACAAGIAIIGGGGAAAGCAICGAAGICTCAIGCA 2065
                                                                                                                                                                 TGAAAAGGTC---TICTICTGAAATAAAGACTGACTACCTATCAATTAAATGGACCCAG 754
                                                                                                                                                398 ATGCTAATGGTGTGCCGGAGCCTCAGATCACTTGGTTTAAAAACAACAACAAAATACAAC 457
                                                                                                                                                                                                                                                                                                                              578 CAGCATACCTCACTGTTCAAGGAACCTCGGACAAGTCTAATCTGGAGCTGATCACTCTAA 637
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                                                                                       338 ICCIGCGAAACCICAGIGAICACACAGIGGCCAICAGCAGIICCACCACTIIAGACIGIC 397
                                                                                                                                                                                                          458 AAGAGCCIGGAAIIAIIIIAGGACCAGGAAGCAGCACGCIGIIIAIIGAAAGAGICACAG 517
                                                                                                                                                                                                                                                                   518 AAGAGGAIGAAGGIGICTAICACIGCAAAGCCACCAACCAGAAGGGCICIGIGGAAAGII 577
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                              CAGGGGAAGAAATCCTCCAGAAGAAATTACAATCAGAGATCAGGAAGCACCATACC
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                        3023 ACASCIICCAASIGGCTAAGGGCAIGGAGITCIIGGCAICGCAAAGIGJATCCACAGG
                                                                                         ACCIGGCAGCGAGAACATICITITATCIGAGAACAACGIGGIGAAGATTIGIGATTIIG
                                                                                                                  1355 ACASTITICAAGIGGCCAGAGGCAIGGAGTICCIGICITCCAGAAAGIGCAITCAICGGG
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APPLICANT: Homas, Renneth A.
APPLICANT: Mo. Xianzhi
APPLICANT: Mo. Xianzhi
APPLICANT: Tobben, Andrew J.
TILE CF INVENTION: HUMAN RECEPTOR TYROSINE KINASE,
CORRESPONDENCE ADDRESS:
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rro. 19963PV
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COMPUTER: IBM PC compatible
OPERATING SYSIEM: PC-DOS/MS-DOS
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Patent No. 6359115
GENERAL INFORMATION:
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STREET: P.O. BOX 2000
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 732/594-3905
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NAME: Hand, J. Mark
REGISTRATION NUMBER: 36,5
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INFORMATION FOR SEQ ID NO:
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ZIP: C7055-0907
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                                                                                                                Length 4071;
                                                                                                               Score 713.8; DB 4;
Pred. No. 8.5e-212;
0; Mismatches 552;
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34.0%;

Best Local Similarity 65.5%;

Matches 1077; Conservative
SEQUENCE CHARACTERISTICS:
LENGTH: 4071 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                   , MOLECULE TYPE: CDNA
US-09-483-539-1
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ADDRESSEE: American Cyanamid Company
STREET: One Cyanamid Plaza
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Patent No. 576660
GENERAL INFORMATION:
APPLICANT: Terman, Bruce I.
APPLICANT: Carrion, Maguel E.
TILLE OF INVENTION: Identification
TITLE OF INVENTION: Patent Receptor
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COMPUTER: IBM PC compatible
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COMPUTER READABLE FORM:
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SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
PELLING DATE: 25-FEB-1997
                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 33.8%; Score 710.6; DB 1; Best Local Similarity 65.3%; Pred. No. 8.5e-211; Matches 1075; Conservative 0; Mismatches 564;
                                                                                                                                                                    31,298-01
                                                                         PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/930,548
FILING DATE: 23-ROV-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                    30,537
                                                                                                                                                                  REFERENCE/DOCKET NUMBÉR: 31 IELECOMMUNICATION:
                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                          TELEPHONE: 201-831-3244
TELEFAX: 201-831-3305
INFORMATION FOR SEQ ID NO: 7
SEQUENCE CHARACIERISTICS:
                                                                                                                                                                                                                                                          4236 base pairs
                                                                                                                                     NAME: Gordon, Alan M. REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                          nucleic acid
EDNESS: single
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                                                                                                                                                                                                                                                                                                        linear
                                                            CLASSIFICATION:
                                                                                                                                                                                                                                                                                        STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                   NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                CS-08-810-116-7
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                                                                                                                                                         IGTIGAAAGAAGGAGCAACACACAGIGAGCAICGAGCICICAIGICIGAACICCAAGAICC 2665
                                                                                                                                                                                                                                                                                                                                     GAGGGCCICTGATGGTGATTGTTGAATACTGCAAATATGGAAATCTCTCCAACTACCTCA 1114
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                                                                                                          IGCIGAAAGAGGGGGCCACGGCCAGCGAGTACAAAGCTCTGATGACTGAGCTAAAAATCT 994
                                GAGGGCCACTCATGGTGATTGTGGAATTCTGCAAATTTGGAAAACCTGTCCACTTACCTGA
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2666 TCATICATAITGGTCACCATCICAATGTGGTCAACCTTCTAGGTGCCTGTACCAAGCCAG 2725
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                                                                                     2545 TIGAAGCAGAIGCCITIGGAATIGACAAGACAGCAACTIGCAGGACAGTAGCAGTCAAAA 2505
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             2246 AGGCATITITCAIAAIAGAAGGIGCCCAGGAAAAGACGAACTIGGAAAICAIIAITCIAG 2305
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                                                           638 CAIGCACCIGIGIGGCIGCGACICITICIGGCICCIATIAACCCICCIIAICCGAAAAA 597
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                                                                                                                                                                 IGAAAAGGIC---IICIICIGAAAIAAAGACIGACTACCIAICAAIIAIAAIGGACCCA
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Sequence 7, Application US/07930548A
Patent No. 5661301
GENERAL INFORMATION:
APPLICANT: Terman, Miguel E.
TITLE OF INVENTION: Identification of a No. 5861301e1 Human Growth
TITLE OF INVENTION: Lactor Receptor
NUMBER OF SEQUENCES: 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                458 AAGAGCCIGGAATIAITTIAGGACCAGGAAGCACCACGCIGTITATIGAAAGAGICACAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/930,548A
FILING DATE: 23-NOV-1992
                                                                                                                                                                                                                              ADDRESSEE: American Cyanamid Company
STREET: One Cyanamid Plaza
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
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TELECOMMUNICATION INFORMATION:
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MOLECULE TYPE: DNA (genomic)
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INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
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ilarity 65.3%;
Conservative
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STRANDEDNESS: single
                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                       STATE: New Jersey COUNTRY: U.S.A. ZIP: 07470
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Best Local Similarity
Matches 1075; Conserv
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1715 CIGAGTACICIACICCIGAAAICIAICAGAICAIGCIGGACIGCIGGCACAGAGACCCAA 1774
                 1775 AAGAAAGGCCAAGAIIIGCAGAACIIGIGGAAAAACIAGGIGAIIIGCIICAAGCAAAIG 1534
                                                                                 2148 CASTIGATIGATICAGAAIGCCICICIGCAGGACCAAGGCGACIAIGIIIC 22...
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IIILE OF INVENTION: Flk-1 is A Receptor For Vascular
IIILE OF INVENTION: Endothelial Growth Factor
NUMBER OF SEQUENCES: 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  33.8%; Score 710; DB 2; 1
65.0%; Pred. No. 1.6e-210;
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ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
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APPLICATION NUMBER: US 08/193,829
FILING DATE: 09-FEB-1994
AITORNEY/AGENT INFORMATION:
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REFERENCE/DOCKET NUMBER: 7683-060
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US/08/443,861
FILING DATE: 22-MAY-1995
                                                                                                                                              3503 CICAGCAGGATGGCAAAGACTACAT 3527
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WEDIOM TYPE: Floppy disk
COMPUTER: IEB PC compatible
OPERATING SYSIEM: PC-DOS/MS-DOS
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Patent No. 5851999
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TELEPHONE: (212)790-9090
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APPLICANT: Millauer, Birgit
APPLICANT: Gazit, Ayiv
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REGISTRATION NUMBER: 30
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INFORMATION FOR SEQ 1D NO:
SEQUENCE CHARACTERISTICS:
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Best Local Similarity
Matches 1081; Conserw
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RY: U.S.A.
10036-2711
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US-08-443-861-1
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2508 IGGCGAAGAGGGAAGAGGCTCTICATAATAGAAGGTGCCCAGGAAAAGACCAACTT 2567
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                                                      2208 IGCICAAGATAAGAAGACCAAGAAAAGACATIGCCIGGICAAACAGCICAICAICCIAGA 2267
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CAACCACAAAATACAACAAGAGCCIGGAAITATTITAGGACCAGGAAGCAGCACGCIGIT 500
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1338 GGAAGAICIGAITICIJACAGITTICAAGIGGCCAGAGGCAIGGAGIICCIGICIICCAG 1397
                                                                       1578 CAGCACCAAGAGCGACGIGIGGICTIACGGAGTATIGCIGIGGGAAAICTICICCITAGG
                                                       1398 AAAGIGCAITCAICGGGACCIGGCAGCGAGAACAITCITIIAICIGAGAACAACGIGGI
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APPLICANT: Galt, Aviv
TILLE OF INVENTION: F1k-1 IS A Receptor For Vascular
TILLE OF INVENTION: Endothelial Growth Factor
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Renni
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APPLICATION DATA:
APPLICATION NUMBER: 05/08/102 CT
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STREET: 1155 Avenue of the Americas
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COMPUTER: IBM PC compatible
OPERAIING SYSIEM: PC-DOS/MS-DOS
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; Patent No. 6177401
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IELECOMMUNICATION INFORMATION:
IELEPHONE: (212)790-9090
IELEFAX: (212)869-9741
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                                                                                                                                                                                                                                                                                                                                               33.8%; Score 710; DB 4; Length 54 65.0%; Pred. No. 1.6e-210; Live 0; Mismatches 575; Indels
IELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 1:
                                                SEQUENCE CHARACTERISTICS:
LENGIH: 5470 base pairs
TYPE: nucleic acid
SIRANDEDNESS: unknown
                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity 65.0
Matches 1081; Conservative
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                                                                                                                                                        unknown
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LOCATION:
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                                                                                               1158 ACACATGGAGCCTAAGAAAAAAATGGAGCCAGGCCTGGAACAAGGCAAGAACCAAG 1217
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1038 AGCCTGCACCAAGCAAGGAGGGCCTCTGAIGGIGAIIGIIGAAIACTGCAAAIÀIGGAAÀ 1097
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                                                                       TCTCTCCAACTACCTCAAGAGCAAACGTGACTTATTTTTTCTCAACAAGGATGCAGCACT
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                                                                                                         Version #1.25
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                                                                                                                                                                                                           PRICE APPLICATION DATA.
APPLICATION NUMBER: US 07/793,065
FILING DATE: 15-NOV-1991
PRICE APPLICATION DATA:
APPLICATION NUMBER: US 07/728,913
FILING DATE: 28-UN-1991
FRICE APPLICATION DATA:
APPLICATION NUMBER: US 07/679,666
                                                                                                                                             APPLICATION NUMBER: US/07/813,593
FILING DATE: 19920415
CLASSIPICATION: 435
                                                           COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PATENTIN Release #1.0, CURRENT APPLICATION DATA:
COMPUTER READABLE FOLL..
MEDIUM IYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Felt, Irving N.
REGISTRATION NUMBER: 28,601
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO: 3: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                 FILING DAIE: 02-APR-1991 AIIORNEY/AGENT INFORMATION:
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LOCATION:
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APPLICANT: Lemischka, Ihor R.
ITILE OF INVENTICW: TOITFOTENT HEMATOPOLETIC STEM CELL.
TITLE OF INVENTICW: RECEPTORS AND THEIR LIGANDS
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NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: IMCLONE SYSTEMS INCORPORATED
STREET: 180 VARICK STREET

NEW YORK U.S.A. CITY: NEW YORK STATE: NEW COUNTRY: U.S ZIP: 10014

Sequence 3, Application US/07813593 Patent No. 5185438

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                                                                                                                  2610 TATIGICATGGATCCAGATGAATTGCCCTTGGATGAGGGCTGTGAACGCTTGCCTTATGA 2659
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                                                          1458 GAAGAIIIGIGAIIIIGGCCIIGCCCGGGAIAIIIAIAAGAACCCCGAIIAISIGAGAAA 1517
                                        691 CCICCIIAICCSAAAAAIGAAAGGIC---IICIIÇIGAAAIAAAGACIGACIACCIAIC 737
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3567 AACTAGAAIGGGGGCICCIGACIACACIACCCCAGAAAIGIACCAGACCAIGCIGGACIG 3626
                                     1758 CIGGCACASAGACCCAAAAGAAAGGCCAAGAITTGCAGAACTTGTGGAAAAACTAGGTGA 1817
                                                                 APPLICANI: Lemischka, Ihor R.

JILLE OF INVENTION: TOTIPOTENT HEMATOPOIETIC STEM CELL
JILLE OF INVENTION: RECEPTORS AND THEIR LIGANDS
CORRESPONDENCES: 10
CORRESPONDENCE ADDRESS:
                                                                                                                           1818 IIIGCIICAAGCAAAIGIACAACAGGAIGGIAAAGACIACAI 1859
                                                                                                                                                     COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFIWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: ImClone Systems Incorporated SIREET: 180 Varick Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER: TW 81102961
FILING DATE: 15-APR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US PCI/US92/02750
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DAIE: 25-JUN-1992
FRICK APPLICATION DAIA: US PCI/US92/05401
APPLICATION NUMBER: US PCI/US92/05401
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/813,593
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28-JUN-1991
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02-APR-1991
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APPLICATION NUMBER: US UNASSIGNED
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FILING DAIE: 26-JUN-1992
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FILING DATE: 19921119
                                                                                                                                                                                                                                       RESULT 8
US-07-977-451-5
: Sequence 5, Application US/07977451
: Patent No. 5270458
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SEQUENCE CHARACTERISTICS:
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FILING DAIE: 15-NOV-1991
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PRIOR APPLICATION DATA:
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PRIOR APPLICATION DAIA:
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MEDIUM TYPE: Floppy
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FILING DATE: 02-APP
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CLASSIFICATION:
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Pred. No. 4.9e-210;
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Best Local Similarity 65.0%;
Matches 1080; Conservative
                                                           ANTI-SENSE: NO FRAGMENT TYPE: N-terminal
                                                                                                                                                                     sig_peptide
208..254
TYPE: NUCLEIC ACID
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
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265..4308
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LOCATION:
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FEATURE:
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                                                                                                   1038 ASCCIGCACCAAGCAAGGAGGGCCICIGAIGGIGAIIGIIGAAAAACIGCAAAIAIGGAAA 1097
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GACTGAGCTAAAAATCTTGACCCACATTGGCCACCATCTGAACGTGGTTAACCTGCTGGG
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IIILE OF INVENTION: TOITOTEOTENT HEMATOPOIETIC STEM-
IIILE OF INVENTION: RECEPTORS AND THEIR LIGANDS
NOWBER OF SEQUENCES: 4
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ADDRESSEE: IMCLONE SYSTEMS INCORPORATED
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Patent No. 5283354
GENERAL INFORMATION:
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                                                                                                                       OPERATING SYSTEM: PC_DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DAIA:
APPLICATION NUMBER: US/07/946,507
                                                                                                                                                                                                              PRICE APPLICATION DATA:
APPLICATION NUMBER: US/07/813,593
FILING DATE: 24-DDC-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/793,065
FILING DATE: 15-NOV-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/728,913
FILING DATE: 28-JUN-1991
PRIOR APPLICATION NUMBER: US/07/679,666
FILING DATE: 02-APR-1991
APPLICATION NUMBER: US/07/679,666
FILING DATE: 02-APR-1991
ATTORNEY/AGENT INFORMATION:
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                                                                                         IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Feit, Irving N.
REGISTRATION NUMBER: 28,601
REFERENCE/DOCKET NUMBER: LEI
STREET: 180 VARICK STREET
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CLASSIFICATION: 535
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Best Local Similarity
Matches 1080; Conserv
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FEATURE:
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US-07-946-507-3
                                               COUNTRY:
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REGISTRATION NUMBER: 28,601
REFERENCE/DOCKET NUMBER: LEMITELECOMMUNICATION INFORMATION:
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SEQUENCE CHARACTERISTICS:
LENGIH: 5406 base pairs
                                                                                                      212-645-1405
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Best Local Similarity 65.0%
Matches 1080; Conservative
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: LOCATION:
US-08-252-517-5
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3447 CACAATICAGAGGGAIGIGGGCTITCGGIGIGIIGCICGGGAAAIAIIIICCIIAGG 3506
                                                               1638 IGGGICTCCATACCCAGGAGTACAATGGATGAGGACITIIGCAGTCGCCTGAGGGAAGG
                                                                                                          1698 CAIGAGGAIGAGAGCICCIGAGIACICIACICCIGAAAICIAICAGAICAIGCIGGACIG
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TITLE OF INVENTION: TOTIPOTENT HEMATOPOIETIC STEM CELL.
TITLE OF INVENTION: RECEPTORS AND THEIR LIGANDS
NUMBER OF SEQUENCES: 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3687 CCICCIGCAAGCAAATGCGCAGGATGGCAAAGACIAIAI 3728
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1818 ITIGCTICAAGCAATGTACAACAGGAIGGTAAAGACTAGAT 1859
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
FILING DATE: 31-OCI-1994
CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
ADDRESSEE: Imclone Systems Incorporated
STREET: 180 Varick Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
APPLICATION NUMBER: US PCI/US92/02750
FILING DATE: 02-AFP-1992
PRIOR APPLICATION DATA:
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115-NOV-1991
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Patent No. 5548065
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07
FILING DATE: 25-JUN-1992
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: TW 81
FILING DATE: 15-APR-1992
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MEDIUM IYPE: Floppy disk
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APPLICATION NUMBER: US 0'
FILING DATE: 02-APR-1991
ATTORNEY/AGENT INFORMATION:
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APPLICATION NUMBER: U
FILING DATE: 28-JUN-1
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FILING DATE: 15-NOV
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New York
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ZIP: 10014
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2070 CAICTTÉAITGIGGCATTICAGAATGCCTCTCTGCAGGACCAAGGCGACTATGTTIGCTC 2129
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          Length 5406;
                                                                        Indels
33.7%; Score 708.4; DB 1;
65.0%; Pred. No. 4.9e-210;
tive 0; Mismatches 576;
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STEM CELL

INCORPORATED

CORPESPONDENCE ADDRESS: ADDRESSEE: IMCLONE SYSTEMS STREET: 180 VARICK STREET

Patent No. 5521090
GENERAL INFORMATION:
APPLICANT: Lemischka, Ihor R.
IIILE OF INVENTION: IOIPOTENT HEMATOPOIETIC STITILE OF INVENTION: RECEPTORS AND THEIR LIGANDS NUMBER OF SEQUENCES: 6

COMPUTER: IBM PC compatible OPERAING SYSTEM: PC-DOS/MS-DOS SCFIWARE: Patentin Release #1.0, Version #1.25

Floppy disk

COMPUTER READABLE FORM: MEDIUM IYPE: Floppy

NEW YORK : U.S.A.

COUNTRY: U

NEW YORK

SIREEI: CIIY: NE SIAIE: N

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/906,397A
FILING DATE: 19920626
CLASSIFICATION: 536

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/813,593 FILING DATE: 24-DEC-1991 PRIOR APPLICATION DATA: APPLICATION WUMBER: US 07/793,065 FILING DAIE: 15-NOV-1991 PRIOR APPLICATION DATA:

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858 GCCITIIGGAAAAGIGGIICAAGCAICAGCAIIIGGCAIIAAGAAAICACCIACGIGCCG 917
                1518 AGGAGAIACTSGACITCCTCTGAAATGGATGGCTCCCGAATCTAICTITGACAAAAATCTA
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                                                           918 GACTGTGGCTGTGAAAATGCTGAAAGAGGGGGCCACGGCCAGCGAGTACAAAGCTCTGAT
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LEM-3-PPPPPP

REGISTRATION NUMBER: 28,601
REFERENCE/DOCKET NUMBER: LE
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-645-1405

212-645-2054

Feit, Irving N.

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/679,666
FILING DATE: 02-APR-1991
ATTORNEY/AGENT INFORMATION:

APPLICATION NUMBER: "US 07/728,913 FILING DATE: 28:JUN-1991

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2070 CAICHTGAIIGIGGCAHHICAGAAHGCCHCHGCAGGACCAAGGCGACTAIGHHGCHC 2129
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Pred. No. 4.9e-210;
0; Mismatches 576;
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65.0%;
INFORMATION FOR SEQ ID NO. 5: SEQUENCE CHARACTERISTICS:
                                LENGTH: 5406 base pairs
IYPE: NUCLEIC ACID
STRANDEDNESS: single
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Bost Local Similarity 65.0
Matches 1080; Conservative
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208..4308
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208..4311
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                                                                                                          MOLECULE TYPE:
                                                                                                                                                              FRAGMENT TYPE:
                                                                                                                               HYPOTHETICAL:
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                                                                                                                                                                                                                                                         NAME/KEY:
                                                                                                                                                                                                     NAME/KEY:
                                                                                                                                                                                                                                                                    LOCATION
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RESULT 11 US-07-906-397A-5 ; Sequence 5, Application US/07906397A

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FILING DATE: 24-DEC-1991
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2190 GCGCATGGCACCCATGATCACCGGAAATCTGGAGAATCAGAGAACAACCATTGGCGAGAC 2249
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IIILE OF INVENTION: TOTIPOTENT HEMATOPOIETIC STEM CELL
IIILE OF INVENTION: RECEPTORS AND THEIR LIGANDS
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CORRESPONDENCE ADDRESS:
ADDRESSEE: ImClone Systems Incorporated
STREET: 180 Varick Street
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US POT ZIEGO APPLICATION FOR APPLICATION NUMBER: US POT ZIEGO A
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APPLICATION NUMBER: US 07/977,451
FILING DATE: 19-NOV-1992
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APPLICATION NUMBER: US 07/813,593
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FILING DATE: 15-FEB-1995
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COMPUIER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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15-APR-1992
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Sequence 5, Application US/08601891
Patent No. 5747651
GENERAL INFORMATION:
APPLICANT: Lemischka, Ihor R.
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PRIOR APPLICATION DAIA:
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MEDIUM IYPE: Floppy
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FILING DAIE: 15-APR
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65.0%; Pred. No. 4.9e-210;
Live 0; Mismatches 576;
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/793,065
FILING DATE: 15-N0V-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/728,913
FILING DATE: 28-JUN-1991
PRIOR APPLICATION NUMBER: US 07/579,666
FILING DAIE: 02-AFR-1991
ATTORNEY/AGENT INVERFATION:
NAME: Felt, IT'YING N.
REGISTRATION NUMBER: LEM-3-7P
REFERENCE/DOCKET NUMBER: LEM-3-7P
TELECOMMUNICATION INFORMATION:
TELEPRONE: 212-645-1405
ITELEPRONE: 212-645-1405
ITELEPRONE: 212-645-2054
INFORMATION FOR SEQ ID NO: 5:
                                                                                                                                                                                                                                                                      LENGTH: 5406 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
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208..264
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HYPOTHETICAL: NO.
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                                                                                                                                                                                                                                                                                                                                                                                   FRAGMENT TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY:
LOCATION:
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US-08-601-891-5
                                                                                                                                                                                                                                                                                                                        TOPOLOGY:
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2550 carreregracegracerrangesesecarigaasesesaacreaagaeaecracriere 2609
                                                                                         2510 TATTGLAGATCCAGATGCCCTTGGATGAGCTGTGAACGCTTGCCTTTATGA 2659
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2790 AACAGTAGCCGTCAAGATGTTGAAAGAAGGAGCAACACAACAGCGAGCATCGAGCCTCAT 2849
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Pred. No. 4.9e-210;
0; Mismatches 576;
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Best Local Similarity 65.0%;
Matches 1080; Conservative
                                                                        N-terminal
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208..264
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265..4308
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208..4311
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                         HYPOIHETICAL: N
ANTI-SENSE: NO
FRAGMENT TYPE:
    MOLECULE IYPE:
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LOCATION:
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LOCATION:
                                                                                                                                                                                                                                                  NAME/KEY:
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US-09-021-324-5
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3627 CTGCCATGAGGACCCCAACCAGAGACCTCGTTTCAGAGTIGGTGGAGCATTTGGGAAA 3686
                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: TOTIPOTENT HEMATOPOLETIC STEM CELL TITLE OF INVENTION: RECEPTORS AND THEIR LIGANDS
                                                                   1818 TITGCITCAAGCAAATGIACAACAGGAIGGIAAAAGACIACAI 1859
                                                                                           3687 CCICCIGCAAGCAAAIGCGCAGGAIGGCAAAGACIAIAI 14
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                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: Inclone Systems Incorporated STREET: 180 Varick Street
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PRIOR APPLICATION DATA:
PRIOR APPLICATION UNSER: US 07/679,666
APPLICATION NUMBER: US 07/679,666
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APPLICATION NUMBER: US/07/977,451
FILING DATE: 1992-11-19
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PRIOR APPLICATION DAIA:
APPLICATION WUMBER: US 07/906,397
FILING DAIE: 26-JUN-1992
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/813,593
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15-NOV-1991
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                                                                                                                                                                                                                      Sequence 5, Application US/09021324
; Patent NO. 5912133
: GENERAL INFORMATION:
APPLICANT: Lemischka, Ihor R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           E: Floppy disk
IBM PC compatible
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE: 26-JUN-1992 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15-APR-1992
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TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
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APPLICATION NUMBER: US
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APPLICATION NUMBER: 0
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PRIOR APPLICATION DAIA:
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                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES: 1 CORRESPONDENCE ADDRESS:
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CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                  CITY: New York
STAIE: New Yor'
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US-09-021-324-5
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1430 IGGCTGIGCAAGAGGGGAGACGCTCTTCATAATAGAAGGTGCCCAGGAAAAGACGAATI 2489
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             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
CERALING SYSTEM: PC-POS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 708.4; DB 5;
Pred. No. 4.9e-210;
7; Mismatches 576;
                                                                                                    CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCI/US92/02750
FILING DATE: 19920402
                                                                                                                                                                             ATTORNEY AGENT INFO TON
NAME: FEIT, IRVING N.
PEGISTRATION WUMBER: 28,601
REFERENCE/DOCKET NUMBER: LEM-
IELECOMMUNICATION INFORMATION:
TELEPHONE: 212-645-1405
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65.08;
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INFORMATION FOR SEQ ID NO: 7
SEQUENCE CHARACIERISTICS:
LENGIH: 5406 base pairs
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Best Local Similarity
Matches 1080; Conserv
                                                                                                                                                               CLASSIFICATION:
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PCI-US92-02750-7
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2850 GICTGAACICAAGAICCICAICCACAIIGGICACCAICICAAIGIGGIGAACCICCIAGG 2909
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TILLE OF INVENTION: Receptors and Their Ligands
WIMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
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CITY: NEW YORK
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GENERAL INFORMATION:
APPLICANT: LEMISCHKA, IHOR R.
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PCI-US92-02750-7
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2610 TAITGICAIGGAISCAGAIGAAIIGCCCTIGGAIGAGGGCIGIGAACGCTIGCCTIAIGA 2659

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Query Match
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2850 GICIGAACICAAACICCICACAAITGGCAAAITGAAAGCICCIGG
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                                                         858 GCCITITGGAAAAGTGGTTCAAGCATCAGCATTTGGCATTAAGAAATCACCTACGTGCCG
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                                             IIILE OF INVENTION: TOTIPOTENT HEMATOPOIETIC STEM CELL IIILE OF INVENTION: TOTIPOTENT HEMATOPOIETIC STEM CELL IIILE OF INVENTION: RECEPTORS AND THEIR LIGANDS NYMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEFF, TWAT
                                                                                                                                                                                                                                                                                                                                                                                 SYSTEM: PC-DOS/MS-DOS
PatentIn Release #1.0, Version #1.25
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65.0%; Pred. No. 4.9e-210;
live 0; Mismatches 576;
                                                                                                                                                                               ADDRESSEE: IMCLONE SYSTEMS INCORPORATED STREET: 180 VARICK STREET
                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/05401
                     Sequence 5. Application PC/TUS9205401 GENERAL INFORMATION:
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IBM PC compatible
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-645-1405
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NAME: Feit, Irving N.
REGISTRATION NUMBER: 28,6
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NUCLEIC ACID
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGIH: 5405 base pairs
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30; Conservative
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Search completed: December 8, 2002, 12:53:53 Job time : 179.57 secs

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Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder; ss.
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pTK gene SAL-S1. Protein tyrosine-k Bovine c-Kit bK-1 Human c-Kit oncoge

New isolated polynucleotide and encoded polypeptides, useful in

2001-539352/73

P-PSDB; ABG06099

A novel type III R Buman KDR genomic Murine foetal live

Result No.

Human soluble vasc Nucleotide sequenc pD10-sFlt-1 vector

Soluble VEGF recep

SVEGF-RI gene.

CDNA encoding amin Flt-lextraFAStm/cy Human polynucleoti Human Flt4/VEGFR-3 Human Flt4/VEGFR-3

Human Flt4 recepto Human tyrosine kin Protein tyrosine-k Human Flt4 recepto Human tyrosine kin Plasmid pRK5.tkl-1 Nucleotide sequenc Human soluble VEGF

FLT4 receptor tyro

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flk-1 cDNA sequenc

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Human soluble vasc Human VEGF recepto

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Human flk-1 coding Murine flk-1 cDNA. receptor prot e flk-1 cDNA. Murine flk-1 recep Sequence of murine

Mouse flk-1

Murine flk-1 cDNA. Murine flk-1 cDNA

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diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess Claim 1; SEQ ID No 5090; 103pp; English

The invention relates to isolated polynuclectide (I) and pulpeptide (II) sequences. (I) is useful as hybridisation probes, or polymersec chain reaction (PCR) primers, oligomets, and for chromosome and gene mapping, and in recombinant production of (II). The condition of (III). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (II) and its binding partners are useful in medical disorders involving aberrant protein expression or biological activity. C diagnostics, forensics, gene mapping, identification of mutations cresponsible for genetic disorders or other traits to assess biodisersity and to produce other types of data and products dependent on DNA and and and agnostic coding sequences of the invention.

C Note: The sequence data for this patent did not appear in the printed of security and the action, but was obtained in electronic format directly from Wipo at ftp.wipo.int/pub/published_pct_sequences. 48888**%**8

Sequence 7680 BP; 2279 A; 1661 C; 1739 G; 2001 T; 0 other;

ċ 2019 2319 2199 240 120 180 300€ 360 0 B 7 540 420 Gaps 1900 TATATCACAGATGTGCCAAATGGGTTTCATGTTAACTTGGAAAAAAGCCGACGAAGGA 2380 CCAGGAAGCAGCACGCTGITIATIGAAAGAGICACAGAAGAGGAIGAAGGIGICIAAICAC GAGGACCIGAAACIGICIIGCACAGIIAACAAGIICIIAIACAGAGACGIIACIIGGAII TCAGGCACCIATGCCTGCAGAGCCAGGAATGTATACACAGGGGAAGAATCCTCCAGAAG AAGGAATTACAATCAGAGATCAGGAAGCACGATACCTGGGAAACCTCAGTGATCAC 1 TATATCACAGAIGIGCCAAAIGGGITICAIGITAACITGGAAAAAAIGCCGACGGAAGGA 181 ATCACTAAGGAGCACTCCAICACTCTTAATCTTACCATCATGAATGTTTCCCTGCAAGAT 2200 AAAGAAATIACAAICAGAGTCAGGAAGCACCAIACCICCIGCGAAACCICAGIGAICAC CAGAICACTIGGIIIAAAAACAACCACAAAATACAACAAGAGCCIGGAATIAITIAGGA CCAGGAAGCACCACGCTGTTATTGAAAGAGTCACAGAAGAGGATGAAGGTGTCTATCAC 541 IGCAAAGCCACCAACCAGAAGGGCICIGIGGAAAGIICAGCAIACCICACIGIICAAGGA ACAGIGGCCAICAGCAGIICCACCACIIIAGACIGICAIGCIAAIGGIGICCCCGAGCCI Query Match 100.0%: Score 2101; DB 23; Length 7680; Best Local Similarity 100.0%: Pred. No. 0; Msmatches 2101; Conservative 0; Mismatches 0; Indels 0; 0 Indels ö : Pred. No. 0; 0; Mismatches 361 19 121 301 421 481 241 CO g ò Q ò QQ ŏ g ò g ò g ò D ΟY g οý g

2859 1020 2979 2559 2619 2799 TACTGCAAATATGGAAATCTCTCCAACTACCTCAAGAGCAAACGTGACTTATTTTTCTC 1140 1260 TCTGAGAACAACGTGGTGAAGATTTGTGATTTTGGCCTTGCCCGGGATATTTATAAGAAC 1500 2679 2739 GIGSTIAACCIGGGAGCCIGCACCAAGCAAGGAGGCCCICTGAIGGIGAIIGTIGAA 1080 AACAASGAIGCAGCACIACACAIGGAGCCIAAGAAAAAAAAAIGGAGCCAGGCCIGGAA 1200 AAGGAGCCCAICACTÁIGGAAGAICTGAITICTTACAGTTTTCAAGTGGCCAGAGGCATG 1380 GAGIICCICICICCAGAAAGIGCAITCAICGGGACCTGGCAGGAGAAACAIICIIIA 1440 3459 1520 TITCAGGNAGATAAAAGTCTGAGTGATGTTGAGGAAGGAGGATTCTGACGGTTTCTAC 1320 GAGIICCIGICIICCAGAAAGIGCAIICAICGGGACCIGGCAGCGGGAAACAIICIIITA 3339 GNAATCIICICCTIAGGIGGGICICCAIACCCAGGAGIACAAATGGAIGAGGACITITGC 1680 096 840 006 CTCTTCTGSCTCCTALTAACCCTCCTATCCGAAAATGAAAGGTCTTCTTCTGAAAA CICIICIGSCICCIATIAACCTCCIIATCCGAAAAATGAAAAGGICTTCTTCTGAAAIA 2740 AAAICACIIGGAAQAGGGGCIIIIGGAAAAGTGGIICAAGCATCAGCATTTGGCATTAAG GAGTACAAAGCTCTGATGACTGAGCTAAAAATCTTGACCCACATTGGCCACCATCTGAAC AAATCACTTGGAAGAGGGGCTTTTGGAAAAGTGGTTCAAGCATCAGCATTTGGCATTAAG AAATCACCIACGIGCCGGACIGIGGCTGTGAAAAIGCTGAAAAGGGGGGCCACGGCCAGC AAGACTGACTATCAATTATAATGGACCCAGATGAAGTTCCTTTGGATGAGCAGTGT GAGTACAAAGCTCTGATGACTGAGCTAAAAATCTTGACCCACCATCTGAAC CAAGGCAAGAAACCAAGACTAGATAGCGTCACCAGCAAGGGAAAGCTTTGCGAGGTCCGGC CAAGGCAAGAAACCAAGACTAGATAGCGTCACCAGCAAAGCTTTGCGAGCTCCGGC CCCGATIAIGISAGAAAGGAGAIACTCGACTTCCTCAAAATGGATGGCTCCCGAATCT AICIIIGACAAAAICIACAGCACCAAGAGCGACGIGIGGICTIACGGAGIATIGCIGIGG GAGCGGCTCCCTTATGATGCCAGCAAGTGGGAGTTTGCCCGGGAGAGACTTAAAACTGGGC 2560 721 841 2920 2980 1021 1081 661 781 961 2860 3340 1141 1321 901 1201 -3100 1251 1381 3280 1441 1501 3400 1561 3450 1521 3520 à q B. QQ Dp 9. Cp Op 5 CD QQ g à 8 õ 50 C 3 ΟŸ CP g 8 g Db ò ö ö g 50 ò Ö g G 8 D. 9

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                                                                                                                                                                                                                                                                                                                                                  HCV: gene expression: oligoribonucleotide: tymour; pathogen; virold: Cytokine; prion; antisense cligonucleotide; virolde; protozoacide; antibacterial; ds.
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unpaired
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AGTCGCCTGAGGGAAGGCATGAGGATGAGAGCTCCTGAGTACTCTACTCCTGAAATCTAT
       GTGGAAAAACTASGTGATTTGCTTCAAGCAAATGTACAACAGGATGGTAAASACTACATC
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                              CCAATCAATGCCATACTGACAGGAAATAGTGGGTTTACATACTCAACTCCTGCCTTCTCT
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                                                                                                                                                                                                                                                                                   ABL91752 standard:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          introducing
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cytostatic;
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complementary with the target gene and has at least one end a single-stranded segment of 1-4 nt. The method provides or oligoribonucleotides for antisense inhibition of gene expression usef e.g. for treating tumours but the oligoribonucleotides may also be directed against genes present in pathogens (e.g. Plasmodium or viruses/viroids, pathogenic on humans, animals or plants) or against
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Gaps
                                                                                                                                                                                          cytokine, Id, developmental or prion genes. The method provides more frective inhibition of gene expression than use of known oligonucleotides, probably because the unpaired overhang increases stability and thus intracellular concentration.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 TATATCACAGAIGTGCCAAATGGGTTTCATGTTAACTTGGAAAAATGCCGACGGAAGGA
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                                                                                                                                                                                                                                                                                                                                                                                                                       DB 24; Length 4017;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2; Indels
                                                                                                                                                                                                                                                                                                                                                    Sequence 4017 BP; 1236 A; 915 C; 903 G; 963 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                   Score 2097.8;
Pred. No. 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                   99.88;
                                                                                                                                                                                                                                                                                                                                                                                                                   Ouery Match
Best Local Similarity 99.99
Matches 2099; Conservative
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	V99	XW Therapy: decembers, and another transmitter, which is the property of the concert brain cancer; inflammation; retinopathy; XW breast cancer; brain cancer; inflammation; rheumatoid arthritis; XW gene therapy; ds. XX Some therapy; ds. XX XX NO9858053-A1.	DE .23-DEC-1998. XX XX XX XX PF 17-JUN-1998. 98WO-US12569. XX XX XX XX XX XX XX XX XX	XX XX Kendall RL, Mao X. Tebben A, Thomas KA; XX XX KPI; 1999-095333/08. DR P-PSDB; AAW80997. XX PI Human receptor tyrosine kinase protein, KDR - useful e.g. to screen PI for antagonists useful to treat diseases involving neoanglogenesis PI e.g. diabetic retinal vascularization, cancers XX	This nucleotide sequence encodes a novel receptor tyrosine kinase, contened KDR (see AARBO97), that is expressed on human endothelial colls. KDR is activated by vascular endothelial growth factor and consideres a mitogenic signal. It is implicated in clinical neoangiogenesis. KDR cDNA was isolated from a human umbilical vein conduction is call lambda phage cDNA library using a 57-6-bp DNA probe conducting product has amino acid differences from the predicted content product has amino acid differences from the previously content.	c Ala), 787 (Gly to Arg), 835 (Asn to Lys), 848 (Glu to Val) and 1347 (Cl Thr to Ser), producing a protein predicted by computer modeling to C (Thr to Ser), producing a protein predicted by computer modeling to C tay higher activity and functionality. The invention also relates CC to recombinant vectors and recombinant hosts which contain a DNA C fragment encoding human KDR, a DNA fragment encoding the C intracellular portion of KDR with or without a membrane anchor C intracellular portion of KDR with or without a membrane anchor C sequence, purified forms of associated human KDR, and human mutant C forms of KDR. KDR, fusion proteins or fragments can be used in C sesays to identify antagonists and agonists of human KDR (claimed).
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0y 841 AAATCACTTGGAAGAGGGCTTTTGGAAAAGTGGTTCAAGCATCAGCATTTGGCATTAAG 900 1H1[H]H]H]H]H]H]H]H]H]H]H]H]H]H]H]H]H]H]	Oy 1081 TACTGCAAATATGGAAATCTCTCCAACTACCTCAAGGGCAACGTGACTTATTTTTTCTC 1140 Db 2731 TACTGCAAATATGGAAATCTCTCCAACTACCTCAACGCGAACGTGACTTATTTTTTCTC 2790 1141 BACAAGGATGCAGAACTTCTCCCAACTAGAAAAAAAAATGGAGCCAGGCCTGGAA 1200 Db 2791 AACAAGGATGCAGACTACACATGGAGCCTAAGAAAAAAAA	1261 INTEGGRACATION AND AND AND AND AND AND AND AND AND AN	Oy 1381 GAGITCCIGITTCCASAAAGIGCAITCATCGGGACCIGGCAGCAACAICITITA 1440 HIHIHIHIHIHIHIHIHIHIHIHIHIHIHIHIHIHIHI	Qy 1501 CCCGATTAIGTGAGAAAGGAGATACTCGACTTCCTCTGAAAIGGATGCTCCGGAATCT 1560 Db 3151 CCCGATTAIGTGAGAAAGGAGATACTCGACTTCCTCTGAAAIGGATGCTCTGAATCT 3210 ' 1561 ATCTTTGACAAAAGGAGATACTCGACTTCCTCTGGAAAIGGATGCTCTGGATCT 3210 D 1561 ATCTTTGACAAAATCTACAGCACCAAGAGCGACGTTGGTCTTACGGAGTATTGCTGTGG 1520 D 1611	1681 AGIGGCJIGAGGGAAGGCAIGAGGAIGAGAGCICCIGAGICTACICTAC	0y 1801 GIGGAAAACIAGGIGAIIIGCIICAAGCAAAIGIACAACGAIGGIAAAGACIACATC 1860

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ide sequence encodes a novel receptor tyrosine kinase, (see AW80997), that is expressed on human endothelial is activated by vascular endothelial growth factor and intogenic signal. It is implicated in clinical series. KDR cDNA was isolated from a human umbilical vein cell lambda phage cDNA library using a 576-bp DNA probe or generated by PCR (see also AAV99850-53). The predicted in generated by PCR (see also AAV99850-53). The predicted fuct has amino acid differences from the previously DR sequence at positions 498 (Ala to Glu), 772 (Thr to I), to Arg), 885 (Aen to Lys), 848 (Glu to Val) and 1347 producting a protein predicted by computer modeling to activity and functionality. The invention also relates introvectors and recombinant hosts which contain a DNA
AIGCCACCICCAIGIIIGAIGACIACCAGGGCGACAGCAGCACICIGIIG 2100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             tyrosine kinase protein, KDR - useful e.g. to screen useful to treat diseases involving neoangiogenesis etinal vascularization, cancers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              yrosine kinase; human; signal transduction;
ijoqenesis; anglogenesis; diabetic retinopathy;
tach cancer; inflammation; rheumatoid arthritis;
act dermatitis; hypersensitivity; antagonist;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             o X, Tebben A, Thomas KA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          tyrosine kinase KDR cDNA.
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Antagonists of KDP useful for treating diseases involving necangiogenesis e.g. diabetic retinal vascularization, cancers (e.g. brain, breast, etc.) and forms of inflammation e.g. rheumathits, psoriasis, contact dermatitis and hypersensitivity reactions. The polynucleotides are useful to screen for KDR
                                                                                                                                                                                                                                                                                                                 218 ICAIGAAIGIIICCCIGCAAGAIICAGGCACCIAIGCCIGCAGAGCCAGGAAIGIAIACA 277
                                                                                                                                                                                                                                                                                                                                                                                                        337
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                                                                                                   antagonists/agonists and for gene therapy (e.g. by introducing a gene portion encoding a RDR protein containing functional ligand binding and membrane anchoring moieties but not tyrosine kinase activity). They are also useful to measure levels of human KDR.
                                                                                                                                                                                                                                     Score 715.4; DB 20; Length 4071;
Pred. No. 8e-207;
0; Mismatches 561; Indels 6;
                                                                                                                                                                                                  Sequence 4071 BP: 1169 A: 894 C: 1027 G: 981 T: 0 other:
                                                                                                                                                                                                                                       34.1%;
65.5%;
                                                                                                                                                                                                                                                         Best Local Similarity 65.5 Matches 1078; Conservative
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HIV: HCV: gene expression; oligoribonucleotide; tumour; pathosen;
Hium; virus; viroid; cytokine; prion; antisense oligonucleotide;
Hid: virucide; protozoacide; antibacterial; ds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CICIGAAAIGGGIGGCICCCGAAICIAICTITGACAAAAICIACAGGACCAAGGAGGGAGG 1534
                                                                                                                                                                                                                                                                                                                                                                                                                                       SCCITGCCCGGGATATITATAAGAACCCCGATTATGTGAGAAAAGGAGATACTCGACTTC 1534
                                                                                                                                                                                                         2903 STAGCCAGACTCAGCCAGCTCTGGATTTGTGGAGGAGAAGTCCCTCAGTGATGTAGAAG 2952
                                                                                                                                                                                                                                                                        2953 AAGAGGAAGCICCIGAAGAICIGIAIAAGGACIICCIGACCIIGGAGCAICICAICIGII 3022
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                                                                         2785 SSASCAASAANGAATITGTCCCTACAAGACCAAAGGGGCACGATTCCGTCAAGGGA
                                                                                                           1175 AASAAAAATGGAGCCAGGCCIGGAACAAGGCAAGAAACCAAGACIAGAIAGCGICACCA
                                                                                                                               2845 AASACIACGIIGGAGGAAICCCIG---IGGAICIGAAAGGGGGGTIGGACAGCAICACCA
                                                                                                                                                                                                                                                                                                          3202 CTITGAAAIGGAIGGCCCCAGAAACAAIITIIGACAGAGIGIACACAAAICCAGAGIGACG
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The invention relates to a method for inhibiting expression of a target gene (ABL91688-ABL91797) in a cell by introducing at least one office that has a double-stranded structure consisting of a most 49 sequential nucleotide pairs, with at least part of one strand complementary with the target gene and has at least one end a single-stranded segment of 1-4 nt. The method provides oligoribonucleotides for antisense inhibition of gene expression useful e.g. for treating tumours but the oligoribonucleotides may also be directed against genes present in pathogens (e.g. plasmodium or viruses/viroids, pathogenic on humans, animals or plants) or against cross present in pathogens (e.g. plasmodium or cytokine, Id, developmental or prion genes. The method provides more effective inhibition of gene expression than use of known oligonucleotides, probably because the unpaired overhang increases stability and thus intracellular concentration.
                                                                                                                                                                                                                                                               Inhibiting gene expression in cells, useful for e.g. treating tumors, by introducing double-stranded complementary oligoRNA having unpaired terminal bases.
                                                                                                                                                                                  Hadwiger
                                                                                                                                                                                                                                                                                                                                                  Claim 13; Page 67-58; 104pp; German.
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                                                             09-JAN-2001; 2001DE-1000585
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                   11-APR-2002
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iQ T)

34.0%; Score 713.8; DB 24; Length 4044; 65.5%; Pred. No. 2.4e-206; ive 0; Mismatches 562; Indels 6; Sequence 4044 BP; 1163 A; 885 C; 1021 G; 975 T; 0 other; Matches 1077; Conservative Local Similarity Query Match

2006 TCACAGGAAACCTGGAGAAICAGACGACAAGTATTGGGGAAAGCAICGAAGTCTCAIGCA 2065 2126 AAGACTCAGGCATTGTATTGAAGGATGGGAACCGGAACCTCACTATCCGCAGAGTGAGGA 2185 2186 AGGAGGACGAAGCCTCTACACCTGCCAGGCATGCAGTGTTCTTGGCTGTGCAAAAGTGG 2245 2306 TAGGCACGCCGGGATIGCCAIGIICTICIGGCIACTICTIGICAICAICCIACGGACCG 2365 CAGCATACCTCACTGTTCAAGGAACCTCGGACAAGTCTAATCTGGAGCTGATCACTAA 637 CATGCACCTGTGTGGCTGCGACTCTTCTGGCTCCTATTAACCCTCCTTATCCGAAAAA 697 218 TCAIGAAIGITICCCIGCAAGAIICAGGCACCIAIGCCIGCAGAGCCAGGAAIGIAIACA 277 Gaps 278 CAGGGGAAGAAATCCTCCAGAAGAAATTACAATCAGAGATCAGGAAGCACCATACC TCCTGCGAAACCTCAGTGATCACAGTGGCCATCAGCAGTTCCACCACTTTAGACTGTC 398 AIGCIAAIGGIGICCCCGAGCCICAGAICACIIGGIIIAAAAACAACAACAAAAIACAAC 2066 CGCCATCTGGGAATCCCCCTCCACAGATCATGTGGTTTAAAGATAATGAGACCCTTGTAG AAGAGCCTGGAATTATTTTAGGACCAGGAAGCAGCACGCTGTTTATTGAAAGAGTCACAG 338 458 g q õ g S ò g OY g ò g ò οž ò

698 IGAAAAGGIC---ITCIICIGAAAIAAAGACIGACIACCIAICAAIIAIAAAIGGACCCAG 754

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2845 2726 GAGGGCCACTCATGGTGGAATTCTGCAAATTTGGAAACCTGTCACTTACCTGA 2785 GAGGGCCTCTGATGGTGATTGTTGAATACTGCAAATATGGAAATCTCTCCAACTACCTCA 1114 1115 AGAGCAAACGIGACIIATITITICICAACAAGGAIGCAGCACIACACAIGGAGCCTAAGA 1174 AAGAGGAGGATTCTGACGGTTTCTACAAGGAGCCCATCACTATGGAAGATCTGATTTCTT 1354 2953 AAGAGGAAGCTCCTGAAGATCTGTATAAGGACTTCCTGACCTTGGAGCATCTCATCTGTT 3022 HILL-II HIHHHI I HIHHHHIHI II II IIHHHIH II HH GCCTTGCCCGGGATATTATAAGAACCCCGATTATGTGAGAAAAGGAGATACTCGACTTC 1534 GCTIGGCCCGGGAIATITATAAAGATCCAGATTATGTCAGAAAAGGAGATGCTCGCCTCC 3202 GAGTACAAATGGATGAGGACTTTTGCAGTCGCCTGAGGGAAGGCATGAGGATGAGAGCTC 1714 CIGASTACTCIACTCCTGAAAICTATCAGATCATGCTGCTGCTGCTGCCACAGAGACCCAA 1774 1775 AAGAAAGGCCAAGATTIGCAGAACTIGIGGAAAAACTAGGIGATTIGCTICAAGCAAAIG 1834 2366 TTAAGCGGCCCAATGGAGGGGAACTGAAGACGCTACTTGTCCATCGTCCAGGATCCAG 2425 AAGAAAAAATGGAGCCAGGCCTGGAACAAGGCAAGAACCAAGACTAGATAGCGTCACCA 1234 SCASCGAAAGCTTTGCGAGCTCCGGCTTTCAGGAAGATAAAAGTCTGAGTGATGTTGAGG 1294 ACCTEGCAGCEAGAAACATTCTTTATCTGAGAACAACGTGGTGAAGATTTGTGATTTTG 1474 ITGCCCGGGAGAGACTTAAACTGGGCAAATCACTTGGAAGAGGGGCTTTTGGAAAAGTGG 874 CITIGAAAIGGAIGGCCCCAGAAACAAIIIIIGACAGAGIGIACACAAICCAGAGIGAGG GGAGCAAGAGAAATGAATTTGTCCCCTACAAGACCAAAGGGGCACGATTCCGTCAAGGGA ACAGITITICAAGTGGCCAGAGGCATGGAGTTCCTGTCTTCCAGAAAGTGCATTCATCGGG CICTGAAATGGATGGCTCCCGAATCTATCTTTGACAAAATCTACAGCACCAAGAGCGACG TGTGGTCTTACGGAGTATTGCTGTGGGAAJCTTCTCCTTAGGTGGGTCTCCATACCCAG 3383 CIGATTAIACIACACCAGAAAIGTACCAGACCAIGCIGGACIGCIGGACGGGGGGGCCCA 755 AIGAAGIICCIIIGGAIGAGCAGIGIGAGCGGCTCCCITAIGAIGCCAGCAAGIGGGAGI 2426 AIGAACTCCCAITGCAIGAACAITGTGAACGACIGCCITAIGAIGTGCCAAAIGGGGAAI IICAAGCAICAGCAIIIGGCAIIAAGAAAICACCIACGIGCCGGACIGIGGCTGIGAAAA IGCIGAAAGAGGGGGCCACGGCCAGCGAGIACAAAGCICIGAIGACIGAGCIAAAAATCI 2845 2903 (3293 1595 1715 1235 1295 3023 1415 1535 1175 3083 1475 3143 933 2506 995 QQ g g 임 Op 9 Dp 9 g ö d ò Db õ q ó QQ 8 qq ò ŏ g g qq QY δy ద õ 6 õ ò 9 õ ó

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2305 TAGGCACGCGGGGATIGCCAIGTICITGGGCTACTTCTTGCCATCCTACGACGC 2365
             2366 TTAAGCGGGCCAATGGAGGGAACTGAAGACAGGCTACTTGTCCATCGTCATGGATCCAG 2425
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                                                                                    398 AIGCIAAIGGIGICCCCGGAGCCICAGAICACTIGGITIAAAAACAACCACAAAAIACAAC 457
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention relates to a method for inhibiting expression of a target gene (AB191658-AB191797) in a cell by introducing at least one oligoribonocleotide that has a double-stranded structure consisting of at most 49 sequential nucleotide pairs, with at least part of one strand single-stranded segment of 1-4 nt. The method provides single-stranded segment of 1-4 nt. The method provides oligoribonocleotides for antisense inhibition of gene expression useful e.g. for treating tumours but the oligoribonucleotides may also be directed against genes present in pathogens (e.g. plasmodium or viruses/viroids, pathogenic on humans, animals or plants) or against cytokine, id, developmental or prion genee. The method provides more effective inhibition of gene expression than use of known
                                                                                                                                                                                                                                                                                                                                                                                                                            Human; HIV; HCV; gene expression; oligoribonucleotide; tumour; pathogen; Plasmodium; virus; viroid; cytokine; prion; antisense oligonucleotide; cytostatic; virucide; protozoacide; antibacterial; ds.
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3443 GTCAGAGACCCACGITITCAGAGIIGGIGGAACAİTIGGGAAAICICTIGCAAGCIAAIG 3502
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Inhibiting gene expression in cells, useful for e.g. treating tumors, by introducing double-stranded complementary oligoRNA having unpaired
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               278 CAGGGGAAGAAJICCICCAGAAGAAAJIACAAJICAGAGATCAGGAAGCACCAJACC 337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          218 TCATGAAIGTITCCCTGCAAGAITCAGGCACCIAIGCCIGCAGAGCCAGGAAIGIAIACA, 277
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 oligonucleotides, probably because the unpaired overhang increases stability and thus intracellular concentration.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
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                                               1835 TACAACAGGAIGGIAAAGACIACAI 1859
                                                                                 3503 CICAGCAGGATGGCAAAGACIACAI 3527
                                                                                                                                                                                                                                                                                                                                                                               Human polynucleotide SEQ ID NO 97
                                                                                                                                                                                                                                BP.
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Matches 1077;
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binding to a receptor protein complex comprising a vascular endothelial growth factor receptor-2 (VEGFR-2) receptor protein and a neuropilin-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2494
                                                                                    (NP-1) receptor protein. One method comprises introducing a sample comprising the compound to the receptor protein and allowing the compound to bind to the complex. Signaling through VEGRR-2 is enhanced in the presence of the NP-1 co-receptor. The methods of the invention can be used for identifying novel pro- and anti-angiogenic compounds. The present sequence represents the DNA encoding a human VEGRR-2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TCCCCAGAGACCGCTGAAGCCTCTTGGCCGTGGTGCCTTTGGCCAAGTGA 2614
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                                                                                                                                                                                                                                                                                                                                           1955 TIAAGAAIGCATCCTTGCAGGACCAAGGAGACTATGTCTGCCTTGCTCAAGACAGGAAGA 2014
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                                                                                                                                                                                                                                                                                                            ICAIGAAIGTIICCCIGCAAGATICAGGCACCTAIGCCIGCAGAGCCAGGAAIGIATACA 277
                                     invention relates to determining whether a compound is capable
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AIGAAGIICCIIIGGAIGAGCAGIGIGAGCGGCICCCITAIGAIGCCAGCAAGIGGGAGI
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                                                                                                                                                                                                                                          Score 713.8; DB 22; Length 4225;
Pred. No. 2.5e-206;
0; Mismatches 562; Indels 6;
                                                                                                                                                                                                           Sequence 4225 BP; 1204 A; 940 C; 1067 G; 1014 T; 0 other;
 Example 1; Page 32-39; 82pp; English.
                                                                                                                                                                                                                                           34.0%;
65.5%;
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Matches 1077; Conservative
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Best Local &
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3083 ACCIGGCGGCACGAANINICCICIIAICGGAGAAGGAAGGTGGTIAAAAICIGIGACIIIG 3142
                                                                                                                      3203 CTTIGAAATGGGIGGCCCGGAACAATTTTTGACAGGGGACACAATCCAGAGTGACG
                                                                                                                                                                                         3323 GGGIAAAGAIIGAIGAAGAATITTGTAGGCGATTGAAAGAAGGAACIAGAATGAGGCCCC
                                                                                                                                                                                                                                                                                                                              GCCTTGCCCGGGATATITATAAGAACCCCGATTATGTGAGAAAAGGAGATACTEGACTTC
                                                      3143 GCTTGGCCCGGGATAITATAAAGATCCAGATIATGTCAGAAAAGGAGATGCTCGCCTCC
                                                                                                                                                                         IGIGGICTIACGGAGIATIGCIGIGGGAAATCTICICCITAGGIGGGICCATACCCAG
                                                                                                                                                                                                                                           GAGTACAAATGGATGAGGACTTTTGCAGTCGCCTGAGGGAAGGCAIGAGGATGAGAGCTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Determining compounds which bind to a complex comprising vascular endothelial growth factor receptor-2 and Neuropilin-1 to provide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Receptor protein, vascular endothelial growth factor receptor-2; VEGFR-2; neuropilin-1; NP-1; co-receptor; human; anglogenic; ds.
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                                                                                                                                                                                                                       AAGAGGAGATTCTGACGGTTTCTACAAGGAGCCCATCACTATGGAAGATCTGATTTCTT 1354
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             2795 GAGGGCCACTCALGGGGATTGTGCAAATTGGAAACCTGTCCACTTACCTGA
                                                                                                                            2915 AAGACIAGGIIGGAGGAAIGCCIG---IGGAICIGAACGGCGCIIGGACAGCAICACCA
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                                                                                 2855 GGAGCAAGAAATGAATTTGTCCCCTACAAGACCAAAGGGGCACGATTCCGTCAAGGGA
                                                                                                                                                                    GCAGGGAAAGCITTGCGAGCTCCGGCTTTCAGGAAGATAAAAGTCTGAGTGATGTTGAGG
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                                                     1115 AGAGCAAACGTGACTTATTTTTCTCAACAAGGATGCAGCACTACACATGGAGCCTAAGA
                                                                                                             1175 AAGAAAAATGGAGCCAGGCCTGGAACAAGGCAAGAAACCAAGACTAGAIAGCGTCACCA
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gene. A labelled EcoRI-BamHI DNA segment derived from clone BTIII081.8

was used as a probe to rescreen a human endothelial cound library

(#110245) for 5'full length DNA segment of the gene from which the
insert portion of BTIII081.8 is derived. A synthetic probe designed

from uniquedides 3297-3325 of BTIII081.8 is then used to isolate

more 3 full length clones. One of the clones, designated BTIII200.2

is cloned into pBluescript KS and the synthetic oligonucleotide

ICGACGCCG AIG GAG cloned, which contains the initial sequence Met
Glu. the first two amino acids encoded by the KDR gene, forming

BILVI-10, which is then purified on a Cscl density gradient. This

was sequenced, together with BIIII081.8, and BTIII129.5 to comprise

the entire ORE of 4,068 nucleotides of the KDR gene.

BTII1081.8

for

DNA encoding type III receptor tyrosine kinase - useful diagnosing the onset of cancer

(AMCY) AMERICAN CYANAMID CO

Carrion ME, Terman Bl; WPI: 1992-315117/38. P-PSER: AAR26999.

92WO-US01300 91US-0657236.

20-FEB-1992; 22-FEB-1991; Claim 3; Fig 7; 101pp; English.

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CACAGGAAACCIGGAGAAICAGACGACAAGIAIIGGGGAAAGCAICGAAGICICAIGCA 2065
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33.8%; Score 710.6; DB 13; Length 4071; 65.3%; Pred, No. 2.3e-205;
                                                    0; Mismatches 564;
                           Best Local Similarity 65.3
Matches 1975; Conservative
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tumour; diagnosing; monitoring; ss.
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15-FEB-1993

AAQ28272;

Homo sapiens

Receptor cancer:

2;

Indels

Sequence 4071 BP; 1172 A; 894 C; 1024 G; 981 I; 0 other;

Query Match

Page 10

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1775 AAGAAAGGCCAAGATTTGCAGAACTTGTGGAAAAACTAGGTGATTTGCTTCAAGCAAATG 1834
                                                                              3443 GICAGAGCCCACGIIICAGAGIIGGIGGAACAIIIGGGAAAICTCIIGCAAGCIAAIG 3502
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     218 ICAIGAAIGITICCCIGCAAGAIICAGGCACCIAIGCCIGCAGAGGCAGGAAIGIAIACA 277
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                                                                                                                                                                                                                  screening; inhibitor;
                                                                                                                                                                                                               Kinase insert domain containing receptor; KDR; screening; inhibito vascular endothelial growth factor; VEGF; angiogenesis; treatment;
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AAV34763 standard; DNA; 4236
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97US-0810116.
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Matches 1075; Conservative
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                                                                                                                                                             Human KDR genomic DNA
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                                                                                                                                                                                                                                                                                                                        Homo sapiens
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                                                                                                         27-AUG-1998
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45 CCAAGAAAGGCAIIGGGIGGICAGGCAGCICAGGICCIAGAGCGIGIGGCACCCACG 38 ICCTGCGAAACCTCAGTGAICACACAGTGGCCATCAGCAGTTCCACCACGTTTAGAATTTAGAATTTAGAATTTAGAATTTAGAAAAGAAAGATCAGAAGTTCAGTGAAAGATAGAAAGAA	458 AACACTIGGAATIATITIAGGACCAGCAGCAGCGCGTTTATIGGAAGAGTCACAG 2125 AACATCAGGATTATITIAGGACCAGCAGCAGCCGTTTATIGGAAGAGTCACAG 2126 AACATCAGGCATTATITIAAGGACTGCAGAACCTCACCACCACCACCAGGGTGGGAA 518 AACAGATGAAGGTCTACACTGCAGAGAACCTACCAACCAA	638 CATGCACCTGTGGGCGGCGCCTCTTCTGGCTCCTATTAACCCTCCTTAICCGAAAAA 1 1 1 1 1 1 1 1 1 1	15 7 86 46 46	935 IGCTGAAAGAGGGGGCAGGGCAAAAAGTGTGAAAATGT 2605 IGTTGAAAGAGGGGGCACGAAAAAAGTGTAAAATGT 2605 IGTTGAAAGAAGGAAGCAACAAGTGGAGCTACATGTGTGAAATGT 995 IGACCCACTTGGCCACCATCTGAACGTGGTTAACCTGCTGGAGACCTGAACAAGAAG 995 IGACCCACTTGGCCACCATCTGAACGTGGTTAACCTGCTGGAGACCTGCACAAGAAG 1	1115 AGAGGAAACGTGACTIAITITICTCAACAAGGATGCAGCACTACACATGGAGCTAAGA	1295 AAGAGGAGGATICTGACGGTTTCTACAAGGAGCCATCACTATGGAAGATCTGATTTCTT
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3383 CIGALIAIACTACACCAGAAAATGTACCAGACCATGCTGGACTGCTGGCACGGGGGAGCCCA 3442
                                                                                                                                                                                                                                                                                                       3443 GTCAGAGGCCACGTITTCAGAGTTGGTGGAACATTTGGGAAATCTCTTGCAAGCTAATG 3502
                                              3203 CITIGAAAIGSAIGGCCCCAGAACAAITIIGACAGAGGIACACAAICCAGAGIGACG 3262
                                                                                                                                                                                          1655 GAĞIACAANIGGAIGAGGACITIIGCAGICGCCIGAGGGAAGGCAIGAGGAIGAGAGCIC 1714
                                                                                                                                                                                                       3323 GGGIAAAGAIIGAIGAAAGAATITIGIAGGCGATIGAAAGAAGGAACTAGAAIGAGGGCCC 3382
                                                                                             1535 CICTGAAATGGATGGCTCCCGAATCTATCTTTGACAAAATCTACAGGACCAAGAGCGACG 1594
                                                                                                                                                          1715 CIGAGIACICIACICCIGAANICIAICAGATCAIGCIGGACIGCCACAGAGACCCAA 1774
                                                                                                                                                                                                                                                                                          1775 AAGAAAGGCCAAGAIIIGCAGAACIIGIGGAAAAACIAGGIGAIIIGCIICAAGCAAAIG 1834
                                                                                                                                            1595 IGIGGICIIACGGAGTALIGCIGIGGGAAATCTICTCCTIAGGIGGGTCTCCCAIACCCAG 1554
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Murine; foetal liver kinase 1; flk-1; protein tyrosine kinase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     monoclonal; antibody; extracellular domain; receptor assay; haematopoietic stem cell: ligand; stimulation; proliferation; differentiation; reatment; anaemia; bone marrow damage; cancer chemocherapy; radiation; ds.
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265..4308
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02-APR-1991;
28-JUN-1991;
15-NOV-1991;
24-DEC-1991;
25-JUN-1992;
12-NOV-1992;
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                                                                                                                                                                                                                                                                                                                                                                                The present sequence encodes murine foetal liver kinase 1 (flk-1), a protein tyrosine kinase. Isolated antibodies, pref. monoclonal, raised against the extracellular portion of flk-1 can be used to assay for flk receptors on the surface of haematopoietic etem cells, and to isolate positive cells. The antibodies can also be used as, or to obtain ligands, which stimulate the proliferation and/or differentiation of stem cells. The ligands can be used, e.g. for treating anaemia, or bone marrow damage resulting from cancer
                                                                                                                                                                                                                                      Anti-foetal liver kinase 2 (fik-2) antibodies - useful in assays, for isolating haematopoietic stem cells expressing receptor and for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2190 GCGCATGGCACCCATGATCACCGGAAATCTGGAGAATCAGACAACAACAACCATTGGCGAGAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            33.7%; Score 708.4; DB 17; Length 5404; 65.0%; Pred. No. 1.3e-204; Live 0; Mismatches 576; Indels 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 5404 BP; 1411 A; 1297 C; 1423 G; 1273 I; 0 other
                                                                                                                                                                                                                                                                                                                                  Disclosure; Columns 51-62; 50pp; English.
93US-0055269
94US-0252517
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   chemotherapy, or radiation
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                                                                     (UYPR-) UNIV PRINCETON.
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                                                                                                                                                                                                                                                                                       obtaining ligands
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                                                                                                                   Lemischka IR;
30-APR-1993;
31-OCT-1994;
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                                                                                                                                                                                                                                                                                                                                          GACTGAGCTAAAAATCTTGACCCACATTGGCCACCATCTGAACGTGGTTAACCTGCTGGG
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                                                                                         GCCTTTTGGAAAAGTGGTTCAAGCATCAGCATTTGGCATTAAGAAATCACCTACGTGCCG
                                                                                                                                                 2730 IGCCTTCGGCCAAGTGATTGAGGCAGACGCTTTTGGAATTGACAAGACAGCGACTTGCAA
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1338 GGAAGAICIGAIIICIIACAGIITICAAGIGGCCAGAGGCAIGGAGIICCIGICTICCAG 1397
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          2190 GCGCATGCCATGATCACCGGAAATCTGGAGAAATCAGACAATTGGCGAGAC 2249
                                                                            2490 GGAAG:CAIIAICCICGICGGCACIGCAGIGAIIGCCAIGIICIICUIGGCICCIICIIGI 2549
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                                                                                                                           CAACCACAAAATACAACAAGAGGCTGGAAITATTTTAGGACCAGGAAGCAGGAGGTGII 500.
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                                                         CACCACITIAGACTGICAIGCIAATGGIGTCCCCGAGCCICAGAICACTIGGITTAAAAA 440
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2130 TGCTCAAGAIAAGAAGACCAAGAAAAGACATIGCCIGGTCAAACAGCICAICAICCIAGA 2189
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Isolating hematopoletic cells expressing fetal liver kinase 1
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                                                                                                                                                        Murine; flk-2; flk-1; cell isolation; fetal liver kinase; monoclonal; polyclonal; antibody; tyrosine kinase; ds.
Location/Qualifiers
208..4311
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920S-0906397.
920S-0975049.
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P-PSDB; AAY08618.
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Matches 1080; Conserv
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02-APR-1991;
28-JUN-1991;
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15-FEB-1996;
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26-JUN-1992;
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English
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Best Local Similarity 65.0
Matches 1080; Conservative
                                                                       Disclosure; Fig 2; 60pp;
               WPI: 1993-405021/50
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Lemischka IR;
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                                                               3387 AGGAGAIGCCCGACICCCIITGAAGIGGAIGGCCCGGGAAACCAIIIIIGACAGGIAIA 3446
                                                                                                                1638 TGGGTCTCCATACCCAGGAGTACAAATGGATGAGGACTTTTGCAGTCGCCTGAGGGAAGG 1697
                                                                                                                                                1698 CATGAGGAIGAGAGCICCIGAGIACICIACICCIGAAAICTAICAGAICAIGCIGGACIG 1757
Receptor protein tyrosine kinase; pTK family; foetal liver kinase; mflk; primitive; totipotent; haematopoietic cell; stem cell; proliferation; stromal cell; ds.
                                                                                                                                                         3627 CIGGCAIGAGGACCCCAACCAGAGACCTCGIIIICAGAGIIGGIGGAGCAIIIGGGAAA
                                               AGGAGATACTCGACTTCCTCTGAAAIGGATGGCTCCGGAATCTATCTTTGACAAAÄTCTA
                                                                                        1578 CAGCACCAAGAGGGACGIGIGGICIIACGGAGIAIIGCIGIGGGGAAAICIICTCCIIAGG
                GAAGAITIGIGATTIIGGCCTIGCCCGGGAIATIIAIAAGAACCCCGATIAIGIGAGAAA
                        /*tag= b
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265..4308
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19-NOV-1992;
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28-JUN-1991;
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                                                                                                                                                                                                                                         Nucleic acid sequences coding for murine flk-2 and specified subfragments of it are claimed. The murine flk-1 coding sequence (i.e. AAOSSO4) is also disclosed. The flk polypeptides are receptor protein tyrosine kinases which are expressed only in primitive hematopoletic cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 708.4; DB 14; Length 5406;
Pred. No. 1.3e-204;
0; Mismatches 576; Indels 6;
isolated nucleic acid molecules of hematopoietic stem cell receptor flk-2 - encoding mammalian receptor protein tyrosine kinases expressed in primitive haematopoietic cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 5406 RP; 1412 A; 1298 C; 1423 G; 1273 T; 0 other;
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Human; receptor; protein; tyrosine kinase; pTK; primitive; mammalian; bematopoletic cell; pHC; mature; mHC; fetal; liver kinase 2; flk-1; liver; spleen; thymus; adult; brain; marrow; thymocyte; subset; nultipotential; Tlymphold; lineage; stomach; kidney; lung; heart; intestine; muscle; lymph node; ss.

Location/Qualifiers 208..4311 /*tag= a

Homo sapiens

91US-0728913. 91US-0793065. 91US-0813593. 92WO-US02750.

PRINCETON

(UYPR-) UNIV Lemischka IR:

02-APR-1992;

WPI: 1999-036323/04

P-PSDB; AAR31377

92WO-US05401

25-JUN-1992;

W09300349-A 07-JAN-1993 28-JUN-1991: 24-DEC-1991; 5-NOV-1991;

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Nucleic acid encoding receptor protein tyrosine kinase - development of ligands to stimulate proliferation and/or differentiation of manmalian haematopoietic stem cells

Claim 10; Fig 2: 78pp; English.

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2130 IGCICAAGAIAAGAAGACCAAGAAAAGACATTGCCTGGTCAAACAGCTCATCATCCTAGA 2189
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                                Length 5406;
Seguence 5406 BP: 1412 A: 1299 C: 1422 G: 1273 T: 0 other;
                                33.7%; Score 708.4; DB 14; Length
65.0%; Pred. No. 1.3e-204;
iive 0; Mismatches 576; Indels
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Matches 1080; Conserv
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AAQ35251 standard; cDNA; 5406

RESULT 12 AAQ35251

Human flk-1 coding sequence

25-JUN-1993 AA035251

X EX BX BX BX

5:

Gaps

This sequence encodes a human receptor protein tyrosine kinase which elengst to a new functional class of protein tyrosine kinase (prks). Elengst to a new functional class of protein tyrosine kinases (prks). Elever, this prk is not in the same class as flk-2. Prks in the same class as flk-2 are expressed in primitive mammalian hematopoietic elents but not in mature hematopoietic cells (mHC). This gene is expressed in more mature hematopoietic cells. The protein encoded by this sequence is an example of a receptor prk and is called fetal liver splean. It is to accompanied to the control of the contro

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                                                                                                                                                                                                                                                                                    CIGGCACAGAGACCCAAAAGGAAAGGCCAAGAITIGCAGAACTIGTGGAAAAAACIAGGTGA 1817
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                receptor; protein; tyrosine kinase; pTK; flk-1; flk-2; adult; printlive; hematopoletic cell; mature; fetal; liver; spleen; brain; stomach; kidney; lung; heart; intestine; bone marrow; lymph node; ss
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                                                                                                          IGGGICTCCAIACCCAGGAGIACAAAIGGAIGAGGACTTIIGCAGICGCCIGAGGGAAGG
                                                                                                                                                                                    CATGAGGATGAGAGCTCCTGAGTACTCTACTCCTGAAATCTATCAGATCATGCTGGACTG
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265..4308
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                                                                         9;
                                                  Length 5406;
                  Sequence 5406 BF: 1412 A; 1298 C; 1423 G; 1273 I; 0 other;
                                                                      575; Indels
                                              DB 14;
                                             33.7%; Score 708.4; DB 14
55.0%; Pred. No. 1.3e-204;
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muscle and lymph nodes
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IGCCAGCAAGIGGGAAIICCCCAGGCACCGGCIGAAACIAGGAAAACCICIIGGCCGCG
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                                                  TGCCAGCAAGTGGGGAGTTTGCCCGGGAGAGTTAAACTGGGCAAATCACTTGGAAGAG
                                                                                                                      GGCITITGGAAAAGTGGTTCAAGCATCAGCATTTGGCATTAAGAAATCACCTACGTGCCG
                                                                                                                                                                                         918 GACTGIGGCTGIGAAAAIGCTGAAAGAGGGGGCCACGGCCAGCGAGTACAAAGCTCTGAI
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                                                                                                                                                                                                                                                                                                                                                                                         liver kinase) receptor protein-tyrosine-kinase. Flk1 is expressed in both primitive and mature hematopoietic cells, and in other tissues. The gene product is useful in isolation of receptor ligands, which have applications in diagnosis of bone marrow disorders and in stimulating proliferation and/or differentiation of primitive hematopoietic stem cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       441 CAACCACAAAATACAACAAGAGCCTGGAATTATTTTAGGACCAGGAAGCAGCACGCTGTT
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                                                                                                                                                                                                                                                                                                                                                                          sequence corresponds to a cDNA encoding a mouse Flk1 (fetal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 16; Length 5406;
                                                                                                                                                                                                                                                                  Ligand for receptor protein tyrosine kinase - useful for the
                                                                                                                                                                                                                                                                                  stimulation of primitive haematopoletic stem cells causing proliferation and/or differentiation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          576;
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93US-0157490
                                        94WO-US05944
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                                                                                                                                             (UYPR-) UNIV PRINCETON
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P-PSDB; AAR67817.
                                                                    18-JUN-1993;
21-JUN-1993;
23-NOV-1993;
                                     17-JUN-1994;
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     05-JAN-1995
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Mus musculus adult male lung cDNA, RIXEN full-length enriched
library, clone:1200012B22:FMS-like tyrosine kinase l, full insert
sequence.
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BE030679 128743 MA
AI716140 UI-R-Y0-A
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AL568689 AL568689
AI089100 ou82910.s
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muriase; Musiaus; Musia
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Meth. Enzymol. 303, 19-44 (1999)
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TITLE
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AUTHORS
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AL042601 DKFZp434L
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Copyright (c) 1993 - 2002 Compugen Ltd.
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BG005458 AL575294

827.6 715 571.4 561.4 558.2 466.8

Result . 9 JOURNAL

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DENYSEISKOPITMEDLISYSPOVARGHEFISSRCIHRDLAARNILLSENNVVKICD
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/db_xref="MGD:MGI:55558"
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LKIASKSKERGISDLPRPSFCFSSCGHTRPVQDDESELGKESCCSPPPDYNSVVLYSS
               988 AAAAICIIGACCCACATIGGCCACCATCIGAACGIGGIIAACCIGGIGGGAGCCIGGACC 1047
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data source:MGD, source key:MGI:95555, evidence:iSS
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                           Konno, H., Akiyama, J., Nishi, K., Kitsunai, I., Tashiro, H., Itch, M., Sumi, N., Ishi, Y., Nakhura, S., Matsunai, I., Tashiro, H., Itch, M., Sumi, N., Ishiha, I., Harada, A., Yamamoto, R., Matsunoo, H., Sakajuchi, S., I. Ikagami, I., Kashiraji, K., Fujiwake, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Wataniki, M., Yoneda, Y., Ishikawa, T., Odawa, X., Tanaka, I., Matsunca, S., Karai, J., Kazak, Y., Huramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y. RIKEN integrated sequence analysis (RISA) system-jak-format Genome Res. 10 (11), 1757-1771 (2000)
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Please visit our web site (http://genome.gsc.riken.go.jp/) for
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1 (bases 1 to 936)
                                        1408 CAICGGGACCTGGCAGCGAGAAACATICTTTATCTGAGAACAACGTGGTGAAGAITTGT 1467
                                                                                                1468 GALTITGGCCTTGCCCGGGATATTTATAAGAACCCCGATTAIGTGAGAAAAGGAGAIACI 1527
                                                                                                                                                         CGACTICCTCTGAAAIGGAIGGCICCCGAAICTATCTTIGACAAAAICTACAGCACCAAG 1587
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                                                          1018 ATCAGCCTGGAAAGAATCAAAACCTTTGAGGAGCTTTCACCGAACTCCACCTCCATGTTT.1677
898 AGIGGCTCCACATACTCGACCCCCACCITCTCTGAGGACGCTITGCA 557
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NIH WGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                     GACCCAAAAGAAAGGCCAAGATTTGCAGAACTTGTGGAAAAACTAGGTGATTTGCTTCAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CDNA Library Preparation: Life Technologies, Inc. CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: cgapbs-remail.nih.gov
Tissue Procurement: Life Technologies, Inc.
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/.cce-Torgan: pooled colon, kidney, stomach; Vector:
ENW-SPCRES: Site_1: Not1; Site_2: cccRV (destroyed); RNA
source anonymous pool of 3 colons, age 26 yo male, 49 yo
fomale, 71 yo male colon, 46 yo male kidney, and pool of 2
stomachs, 62 yo male and 70 yo remale. Library is
clips of primed and directionally cloned (RocNv site is
disport primed and directionally cloned (RocNv site is
distroyed upon cloning). Average insert size 1.4 Kb,
miser size range 1.3 Kb. Library is normalized and
clinitody for full-length clones and was constructed by C.
Cluber (Invitroyen). Research Genetics tracking code
(35. Mete this a NIH MCC Library.).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ä
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1425 GAGAAACATTCTTTATCTGAGAACAAGGTGAAGATTTGTGATTTTGGCCTTGCCG 1484
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GAIGGCICCCGANICIATCTTIGACAAAATCTACAGCACGAAGAGGGACGIGGGTCTIA 1604
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114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DNA Sequencing by: Incyte Genomics, Inc.
Close distribution: MGC clone distribution information can if found through the I.M.A.G.E. Consortium/LLML at:
http://imag.ilml.gov.c.column: 24
High quairity sequence stop: 757.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CGGAGIAIIGCINIGGGAAATCITCTCCIIAGGIGGGICICCAIACCCAAGAGIACAAAI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               34.0%; Score 715; DB 13;
99.7%; Pred. No. 8.2e-192;
ive 6; Mismatches 0;
                                                                                                                                                                                                                                                                             /3b_xref="taxxn:9606"
/vione="IMAGE:5188559"
/vlone_lib="NIH_MGC_ll6"
/tab_host="DR108"
                                                                                                                                                                                                                                                /organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity 99.7
17; Conservative
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Cells or adult marrow or brain cells. The PCR primers used are based on known sections of the flk.1 gene. The murine flk.1 clone may be used in a vector to transform haematopoietic cells. The thymidine kinase encoded by fix.1 is expressed in primative but not mature haematapoietic cells. Ligand binding to the TK may be prepd. which haematapoietic cells in Vivo. The ligands can stimulate proliferation and/or differentiation of primative haematapoietic cells in Vivo. The ligands can stimulate the proliferational primitive stem cells, differentiation into
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3355 CCCGACTCCCTTTGAAGTGGATGGCCCGGAAACATTTTGACAGAGTATACACAATC 3454
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  69 CICGACTICCTCTGAAAIGGATGGCICCTGAATCTATCTTIGACAAAATCTACAGCACCA 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Standard PCR techniques from stem-cell receptor-contg. Lissue cDNA librarles. Suitable tissues include foetal liver, spleen or thymus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Receptor protein tyrosine kinase, pTK family, foetal liver kinase, mflk; primitive, totipotent; haematopoietic cell; stem cell; proliferation; stromal cell; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3455 AGAGCGAIGTGIGGGCTTTCGGIGTGTTGCTCTGGGAAAATIIICCTTAGGT 3507
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                                                                                                                                                                                                                                                                                                                                             Stimulating proliferation and/or differentiation of primitive mammalian haematopoietic stem cells - using ligand that binds thymidine kinase and flk-1 and flk-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 5406;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The murine foetal liver kinase (flk) -1 clone was isolated by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 5406 BP; 1412 A; 1294 C; 1427 G; 1273 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 74.6; DB 13
Pred. No. 1.8e-13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         more mature progenitor cells, or both
See also AAQ29954-6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /*tag= a
/product= mflk-1
208..264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAO53504 standard; cDNA; 5406 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 14; Fig 2; 94pp; English.
                                                                                  91US-0679666.
91US-0728913.
91US-0793065.
91US-0813593.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    24.8%;
78.8%;
                                             92WO-US02750
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              27-JUN-1994 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity 78.8 nes 89, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                208..4311
                                                                                                                                                                                             (UYPR-) UNIV PRINCETON
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                                                                                                                                                                                                                                                                           WPI; 1992-366185/44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Murine flk-1 cDNA.
                                                                                                                                                                                                                                                                                                      P-PSDB; AAR28041
                                                                                                         28-JUN-1991;
15-NOV-1991;
24-DEC-1991;
                                                                                                                                                                                                                                           Lemischka IR;
                                           02-APR-1992;
                                                                                    02-APR-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mus musculus.
15-0CT-1992
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Best Local S
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AAQ53504
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XX
XX
XX
XX
FH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         fetal liver kinase 1 (flx.1) receptors on their surface and comprises binding the cells to a polyclonal or monoclonal antibody specific to the Kix-1 receptor and isolating the cells that have bound to the antibody. The method can be used to isolate hematopoletic stem cells in any mammal but preferably a rat, mouse, rabbit or human. The proteins of the invention belong to the receptor protein family. This sequence encodes the murine fix-1 protein which is used in the method of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3395 CCCGACTCCCTTTGAAGTGGATGGCCCGGAAACCATTTTGACAGAGTATACACAATTC 3454
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This invention describes a novel method of isolating cells expressing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       69 CICGACTICCICIGAAAIGGAIGGCTCCTGAATCTAICTTIGACAAAAICIACAGCACCA 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Thymidine kinase; TK; haematopoietic; stem cells; proliferation; differentiation; progenitor cells; foetal liver kinase; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3455 AGAGCGATGTGGGCTTTCGGTGTGCTCTGGGAAATATTTCCTIAGGT 3507
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 5404;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         129 AGAGCGACGTGTCGTCTTACGGAGTATTGCTGTGGGAAATCTTCTCCTTAGGT 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Isolating hematopoietic cells expressing fetal liver kinase 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 5404 BP; 1411 A; 1297 C; 1423 G; 1273 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 74.6; DB 20;
Pred. No. 1.8e-13;
0; Mismatches. 24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; Fig 2; 59pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AA029957 standard; .cDNA; 5406 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0
                                                                                           91US-0679666.
91US-0728913.
91US-0793065.
                                                                                                                                                                                                    92US-0975049.
93US-0055269.
94US-0252498.
96US-0601891.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         24.8%;
78.8%;
                                98US-0021324
                                                                      92US-0977451
                                                                                                                                                           91US-0813593
92US-0906397
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                                                                                                                                                                                                                                                                                                                                                                                                WPI; 1999-357194/30.
P-PSDB; AAY08618.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           flk-1 cDNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
                                                                                                                                                                                                                                                                                                                                                         Lemischka IR;
                             10-FEB-1998;
                                                                                                                                                             1991;
                                                                                                                                                                                                                         30-APR-1993;
31-OCT-1994;
                                                                                                                                                                                1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mus musculus
                                                                      19-NOV-1992
                                                                                                                  28-JUN-1991
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invention.

Query Match

Matches

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receptors

24-DEC-1 26-JUN-1 12-NOV-

WO9217486-A.

AAQ29957;

RESULT 12 AAQ2995

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This sequence encodes a human receptor protein tyrosine kinase which belongs to a new functional class of protein tyrosine kinases (pTKS). However, this pTK is not in the same class as fik-2. pTKS in the same class as fik-2. pTKS in the same class as fik-2 are expressed in primitive mamumalian hematopoietic (pHC) cells but not in marure hematopoietic cells (mHC). This gene is expressed in more mature hematopoietic cells. The protein encoded by this sequence is an example of a receptor pTK and is called fetal liver kinase i (fik-1). fik-1 is expressed in fetal liver.spleen, thymus, brain, stomach, kidney, lung, heart and incestine, and adult brain, kidney, heart, spleen, lung, muscle, marrow and lymph nodes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3395 CCCGACTCCCTTTGAAGTGGATGGCCCGGAAACCATTTTTGACAGAGTATACACAATTC 3454
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   69 CICGACTICCICTGRAAIGGAIGGCICCIGAAICIAICITIGACAAAAICIACAGCACCA 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          receptor; protein; tyrosine kinase; pTK; ilk-1; ilk-2; adult;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              primitive, i.ematopoletic cell; mature; fetal; liver; spleen;
brain; stomack; kidney; lung; heart; intestine; bone marrow;
lymph node; ss
                                                                                                                                                                                                                                                                                                                                                         Nucleic acid encoding receptor protein tyrosine kinase - allows development of ligands to stimulate proliferation and/or differentiation of mammalian haematopoietic stem cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3455 AGAGCGAIGTGTGGTCTTCGGTGTGTGCTCGGGAAAIAIITTCCTIAGGI 3507
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         129 AGAGCGACGIGTGGICTTACGGAGTATTGCTGTGGGAAATCTTCTCCTTAGGT 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 74.6; DB 14; Length 5406;
Pred. No. 1.8e-13;
0; Mismatches 24; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 5406 BP; 1412 A; 1299 C; 1422 G; 1273 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
208..4311
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAQ40916 standard; cDNA; 5406
                                                                                                                                                       910s-0793065.
910s-0813593.
92WO-US02750.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               24.8%;
78.8%;
                                                                                                   92WO-US05401
                                                                                                                                     91US-0728913.
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208..264
/*tag= b
                                                                                                                                                                                                                               (UYPR-) UNIV PRINCETON.
                                                                                                                                                                                                                                                                                                                                                   Nucleic acid encoding
                                                                                                                                                                                                                                                                                                     WPI; 1993-036323/04
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Murine flk-1 cDNA.
                                                                                                                                                                                                                                                                                                                        P-FSDB; AAR31377
                                                                                                                                                                                                                                                                    Lemischka IR;
                                                                                                 26-JUN-1992;
                                                                                                                                     28-JUN-1991;
                                                                                                                                                       15-NOV-1991;
24-DEC-1991;
                       W09300349-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  19-0CT-1593
                                                              67-JAN-1993
                                                                                                                                                                                          02-APR-1992;
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human; receptor; protein; tyrosine kinase; pTK; primitive; mammalian;
hematopoietic cell; pHC; mature; mHC; fetal; liver kinase 2; flk-1;
liver; spleen; thymus; adult; brain; marrow; thymocyte; subset;
multipotential; T-lymphoid; lineage; stomach; kidney; lung; heart;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nucleic acid sequences coding for murine flk-2 and specified subfragments of it are claimed. The murine flk-1 coding sequence (i.e. AQS1504) is also disclosed. The flk polypeptides are receptor protein tyrosine kinases which are expressed only in primitive haematopoletic cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3455 AGAGCGARGTGTGGTCTTCGGTGTTGCTTGGGAAATATTTTCCTTAGGT 3507
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      Isolated nucleic acid molecules of hematopoietic stem cell receptor flk-2 - encoding mammallan receptor protein tyrosine kinases expressed in primitive haematopoietic cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 5406;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 5406 BP; 1412 A; 1298 C; 1423 G; 1273 T; 0 other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 24.8%; Score 74.6; DB 14; 78.8%; Pred. No. 1.8e-13;
/note= "hydrophobic leader"
265..4308
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208..4311
/*tag* a
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; Fig 2; 60pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ВР
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910S-0793065.
910S-0813593.
920S-0906397.
920S-0975049.
920S-0977451.
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                                                                                                                                               910S-0679666
                                                                                                                                                                                91US-0679666
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity 78.8 Matches 89; Conservative
                                    /*tag=
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                                                                                                                                                                                                                                                                                                                                                               Lemischka IR;
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                                                                                                                                           02-APR-1991;
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                                                                                                                                                                              02-APR-1991;
                                                                                                                                                                                                    28-JUN-1991;
                                                                     US5270458-A
                                                                                                                                                                                                                                   24 - DEC - 1991;
               mat_peptide
                                                                                                        14-DEC-1993
                                                                                                                                                                                                                   15-NOV-1991
                                                                                                                                                                                                                                                      26-JUN-1992
                                                                                                                                                                                                                                                                        12-NOV-1992
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Key

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Gaps

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Indels

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This sequence encodes the murine receptor protein tyrosine kinase (PTK), [1k-1]. This pTK is not in the same family as flk-2 (see also AA404091-15) as it is expressed in primitive hematopoietic cells and also in mature hematopoietic cells. flk-1 is expressed in fetal liver, spleen, thymus, brain, stomach, kidney, lung, heart and intestine and adult brain, bone marrow, kidney, heart, spleen, lung, muscle and lymph nodes.
                                                                                                                                                                                                                                                                                     Totipotent haematopoietic stem cell receptors, their ligands and DNA Sequences - for treating anaemia(s) and bone marrow damage due to e.g. cancer chemotherapy or radiotherapy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 5406 BP; 1412 A; 1298 C; 1423 G; 1273 T; 0 other;
/note= "Hydrophobic leader sequence"
265..4308
/*tag= c
                                                                                                                                                                                                                                                                                                                                                   Claim 14; Fig 2; 127pp; English.
                                                                                                                             92WO-US09893.
                                                                                                                                                           910S-0793065
                                                                                                                                                                                     (UYPR-) UNIV PRINCETON.
                                                                                                                                                                                                                                              WPI; 1993-182479/22.
P-PSDB; AAR37504.
                                                                                                                                                                                                                   Lemischka IR;
                                                                                                                             16-NOV-1992;
                                                                                                                                                         15-NOV-1991;
                                                                   WO9310136-A.
                                                                                               27-MAY-1993.
                         mat_peptide
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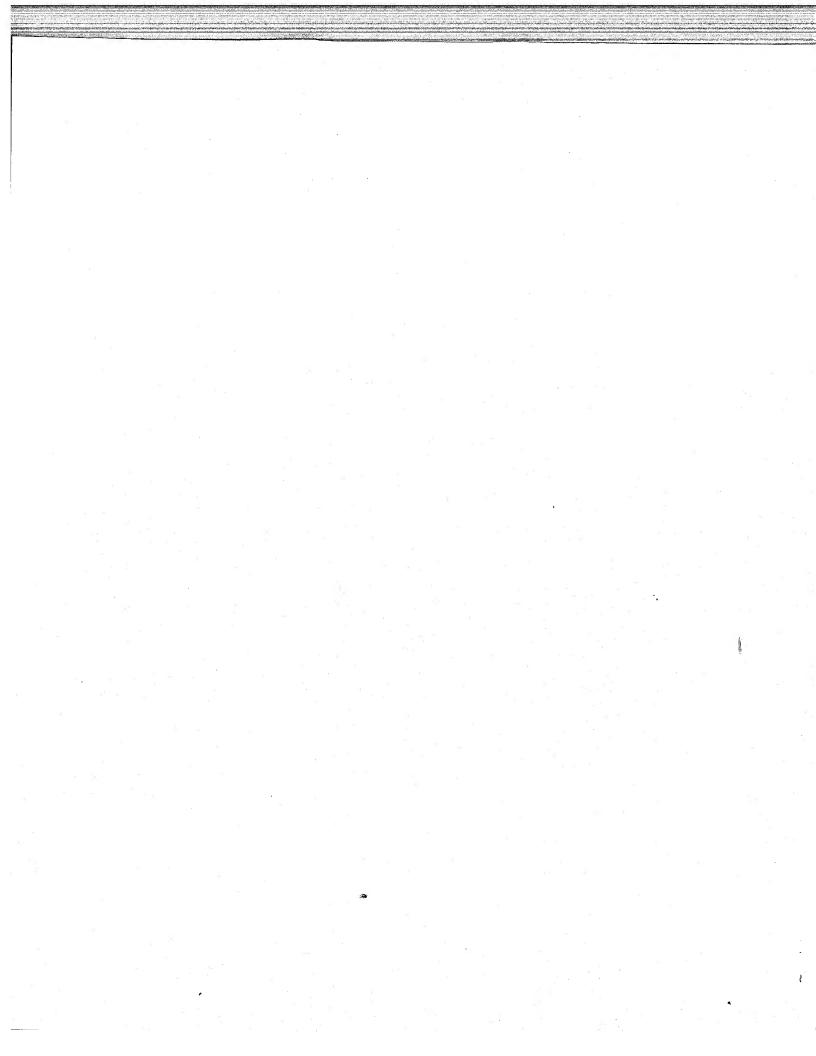
3455 AGAGCGAIGTGIGGTCTTTCGGTGTGTGTCTCTGGGAAATATTTTCCTTAGGT 3507

129 AGAGGGACGTGGTCTTACGGAGTATTGCTGTGGGAAATCTTCTCCTTAGGT 181

Gaps

Score 74.6; DB 14; Length 5406; Pred. No. 1.8e-13; 0; Mismatches 24; Indels 0;

Ouery Match Best Local Similarity 78.8%; Matches 89; Conservative



GenCore version 5.1.3 Copyright (c) 1993 - 2002 Compugen Ltd.

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	s Secc updat	lagt 3						
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OM nucleic - nu	ארט סם:	Title: Perfect score: Sequence:	Scoring table:	Searched:	tal number of	Minimum DB seq length: 0 Maximum DB seq length: 20	Post-processing	Database :

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6: 90_pat:*

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11: 90_oi:*

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12: 90_oi:*

13: 90_oi:*

14: 90_oi:*

15: em_ba:*

15: em_ha:*

16: em_ha:*

20: em_oi:*

21: em_pi:*

22: em_oi:*

23: em_pi:*

24: em_pi:*

25: em_vi:*

25: em_vi:*

26: em_ro:*

27: em_sts:*

28: em_htg_inv:*

31: em_htg_inv:*

32: em_htg_inv:*

33: em_htg_inv:*

34: em_htg_inv:*

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score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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	4 linear PRI 03-AUG-2001	2P18 on chromosome 13.							1; Vertebrata; Euteleostomi:	ini: Hominidae: Homo			
	AL138712 164519 DD DNA	Human DNA sequence from clone RP11-502P18 on chromosome 13.	complete sequence.	AL138712	AL138712.19 GI:15131448	HTG.	human.	Homo sapiens	Eukaryota; Metazoa; Chordata; Craniata; Verlebrata; Euteleostomi;	Mammalia; Eutheria; Primates; Catarrhini: Hominidae: Homo	l (bases 1 to 164519)	Bates, K.	Direct Submission
RESULI 1 AL138712/c	rocus	DEFINITION		ACCESSION	VERSION	KEYWORDS	SOURCE	ORGANISM			REFERENCE	AUTHORS	TITLE

umber of results predicted by chance to have a

em_htgo_mus:* em_htgo_other:* a

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/note="14125/x repeat: matches 75. 133 of consensus" 27339. 27650
/note="AluSp repeat: matches 1. 313 of consensus" 27679. 27810
/note="Single clone region. Sequence from reads from a short insert library derived from a single pUC clone. 87821. 28123
                                                                                                                                                             .6169 of consensus*
                                                                                                                                                                                                        .5477 of consensus
                                                                                                                                                                                                                                                                                                                                      repeat: matches 3892. .4063 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                      .5255 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .i739 of consensus
                                                                                                                                                                                                                                                     .6299 of consensus
                                                                                                                                                                                                                                                                                                                                                                                                                                   .5103 of consensus
                   /note="LIM4 repeat: matches 4612. .4706 of consensus" 12550. .12859 //note="AluSg repeat: matches 1..310 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="FRAM repeat: matches 1. .160 of consensus"
27014. 27230
/note="Alusg/x repeat: matches 89. .305 of consensus"
27233. 27286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           //coce="Aluub repeat: matches 144. 255 of consensus" 18089. 18379
                                                                                                                                                                                                                                                                                                   .301 of consensus*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Anote-"AluSx repeat: matches 1. .352 of consensus" [7794, .17914
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          fnote="AluSq repeat: matches 1. .252 of consensus" 8380. .18516
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .8380 .18516
.mote="AluJo repeat: matches 1. .144 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note-"AluSx repeat: matches 1. .311 of consensus"
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26437. ;26754
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/note="WER2 repeat: matches 2. .344 of consensus"
26845. .27004
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                                                                                                             matches 4344. .4612 of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="11 copies 2 mer tt 100% conserved"
21313. .21486
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            25177. 25343
70ote-Charlie3 repeat: matches 48. .215.
25574. 25557
70ote-82 copies 2 mer ta 61% conserved.
25538. .25830
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ancte-MIR repeat: matches 1. 251 of 24957. 25516 hote="Sequence from clone PCR only."
                                                                                                                                                                                                                    14017. 16233
/note-"LIMA4 repeat: matches 4063.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  note="LIMEc repeat: matches 1622.
7915. 18088
                                                                                                                                                                                                        repeat: matches 5250.
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29773. .29973
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29264. .29564
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13227, 1374^
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/note="AluJb re
16507. .16680
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/note-"LIMB7 r
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17160: .17462
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16589. 1769.
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16910. 1771
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                                                                                                                                                                                                                                                regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality) = 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subotone or more than one MI3 subcione; and the assembly was confirmed by restriction digest. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em. EMBL; Sx.; SWISSPROT: IT: TREMBL; WP: WORMPEP; Information on the WORMPEP database can be found at
                                                                                                                                     together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with a small overlap as described above.
                                      requests: clonerequestésanger.ac.uk
On Aug 9, 2001 this sequence version replaced gi:11715292.
During sequence assembly data is compared from overlapping clones.
Where differences are found these are annotated as variations
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               http://www.sanger.ac.uk/HGP/Chri3
RP11-502P18 is from the library RPCI-11.2 constructed by the group
of Pieter de Jong. For further details see
                                                                                                                                                                                                                             This sequence was finished as follows unless otherwise noted: all
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 13, constructed by the Sanger Centre Chromosome 13 Mapping Group. Further information can be found at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          sections only once, except for a 100 base overlap. The tr.. right end of clone RP11-502718 is at 164519 in this sequence. The true lett end of clone RP11-9566 is at 2000 in this sequence. The true right end of clone RP11-9566 is at 2000 in this sequence.
Submitted (03-AUG-2001) Sanger Centre, Hinxton, Cambridgeshire.
CB10 18A, UK. B-mail enquiries: humqueryésanger.ac.uk Clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1989. .2053
Nocte-"AluJ/FLAM repeat: matches 21. .66 of consensus"
2724. .2892
Nocte-"L2 repeat: matches 2206. .2358 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IMPORTANT: This sequence is not the entire insert of clone RP11-502P18 It may be shorter because we sequence overlapping
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/note="FLAM_C repeat: matches 33. .124 of consensus"
6847. 6934
/note="44_copies 2 mer ca 79% conserved"
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note="MERSA repeat: matches 95. .168 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 83. .1279
note="Alusx repeat: matches 1. .297 of consensus"
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Moote-"U6 repeat: matches 2. .104 of consensus"
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note="22 copies 2 mer ac 93% conserved"
153. 3743
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0814. .10984
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1. .164519
/organism="Homo sapiens"
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/clone_lib="RPCI-11.2"
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'hote="MER5B repeat; 495. .4586
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sequences, will become prior art. Patent and Trademark Office after November 29, 2000 will be pre-published at eighteen months from the effective filing date. When the application is published the contents, including the According to the Pre Publication Rules, every patent application received by the United States

extension .rnpb Published Applications NA contains nucleic acid sequences; the search results will have the Published_Applications_AA contains amino acid sequences; the search results will have the Two new databases have been created to hold the pre-published sequences:

extension .rapb.

digits represent when the application was published. This 7-digit number starts at zero at the application. The first 4 digits show the calendar year the application was published. The next 7 requests that the changed application be published again. In such instances, the "1" at the end of application had been published. If the applicants submit changes to the application, they may beginning of each calendar year. Each application published is given the next number in order Publication Number is US20021234567A1. The "US" indicates the application was a U.S. The "A" indicates a utility patent application and the "1" shows that this was the first time the Each pre-published application is given a unique Publication Number. An example of a the number would be replaced by a "2"

Sequences in the PGPub database are public information; it is permissible to leave these results in the case.

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Copyright (c) 1993 - 2002 Compugen Ltd.
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Description	Sequence 29, Appl Sequence 17, Appl	Sequence 292, App Sequence 529, App Sequence 3950, App			Sequence 50, Appl Sequence 50, Appl Sequence 8, Appli Sequence 292, Appli Sequence 292, Appli Sequence 592, Appli
SUMMARIES	US-09-804-682-29 US-09-814-777A-17	US-09-954-456-292 US-09-954-456-529 US-09-880-107-3950	US-09-799-462A-17 US-10-125-767-17 US-10-023-529-48 US-10-023-523-48	US-09-854-998-35 US-10-023-529-45 US-10-023-523-45 US-09-764-877-2718	US-10-023-523-50 US-09-817-913-8 US-09-817-538-8 US-09-954-456-292 US-09-954-456-292
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Query Match 5.6%; Score 52.6; DB 10; Length 1064; Best Local Similarity 41.5%; Pred. Nc. 0.0047; Matches 15%; Conservative 0; Mismatches 217; Indels 0;

Sequence 3950, App Sequence 399, App Sequence 399, App Sequence 40, Appl Sequence 10, Appl Sequence 11, Appl Sequence 1130, Ap Sequence 1130, Ap Sequence 2109, Ap Sequence 311, Appl Sequence 311, Appl Sequence 31, Appl Sequence 1621, Appl Sequence 1621, Appl Sequence 1624, Appl Sequence 16, Appl	EONING FOR OR	7, 231, 232, 17, 306, 319, 12, 376, 378, 18, 470 16, 687, 691, 17, 687, 691, 17, 852, 1, 852, 743, 1, 852, 18, 1, 1011, 1018,
29.99.90 29.99.90 29.99.90 29.99.90 29.90 29.90 29.90 20.0	TIC ACIES	110, 209, 214 282, 252, 29 355, 363, 37 458, 459, 46 524, 527, 55 654, 674, 68 731, 734, 73 821, 823, 84 7317, 526, 53 1, 1002, 1005, 1005,
US-09-98-107-108-09-978-2558-108-09-978-1928-1928-1928-1928-1928-1928-1928-192	ALIGNMENI 04682 04682 IHE SAME AND 3 THE SAME 709/804,682 12 Version 4.0	25, 33, 39, 72, 245, 256, 256, 454, 454, 454, 454, 454, 454, 456, 499, 511, 426, 499, 511, 623, 624, 652, 726, 729, 803, 799, 991, 993, 100, 991, 993, 1051, 1054, 1055, or G
43056 43	ion US/09 765Al 765Al Ichael J. FAL-18 PO PAL-18 PO PODIA, ONABER: 01.406 1.01.406 2001-03 1.174 1.174 1.174	18. 21, 24, 24, 237, 237, 238, 244, 336, 405, 432, 437, 400, 10, 10, 10, 10, 10, 10, 10, 10, 10,
>=====================================	ESULI 1 5.09-804-682-29/c 5.09-804-682-29/c 6ENERAL INCEMATION: APPLICANT: KINGERS, MAPPLICANT: COPEY, M TITLE OF INVENTION: FILE REFERENCE: 1300 CURRENT FILLING DATE: NUMBER OF SEQ ID NOS SCETTARE: FALSEQ FO SEQ ID NO 29 TYRE: DAA GRACHISM: HOME SAPI, FEE DAA GRACHISM: HOME SAPI, FEE DAA GRACHISM: HOME SAPI, FEE DAA GRACHISM: HOME SAPI, FEE DAA GRACHISM: HOME SAPI, FEE DAA GRACHISM: HOME SAPI, FEE DAA GRACHISM: HOME SAPI, FEE DAA GRACHISM: HOME SAPI, FEE DAA	23. 6. 6. 6. 6. 6. 6. 6. 6. 6. 6. 6. 6. 6.
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APPLICANT: Young, Paul
TITLE OF INVENTION: Process for Identifying Anti-Cancer Therapeutic Agents Using C
TITLE OF INVENTION: Sets
FILE REFERENCE: 689290-76
CURRENT APPLICATION NUMBER: US/09/954,456
CURRENT FILING DAIE: 2001-09-18
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530 CICGICGCCCCCCCCTCTCCGIAGCCGAGGGAAGCGAGCGAGGAAGAAGAGG 579
                                                                    640 GGGIAGGAAGIGGGCIGGGGAAAGGTTATAAATCGCCCCCGCCCTCGGCTGCTTCAIC 699
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Pred. No. 0.02;
0; Mismatches 259;
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PRIOR PILING DATE: 2000-09-20
PRIOR APPLICATION NUMBER: US/60/234, 952
PRIOR APPLICATION NUMBER: US/60/234, 923
PRIOR APPLICATION NUMBER: US/60/235, 134
PRIOR PRILING DATE: 2000-09-25
PRIOR FILING DATE: 2000-09-26
PRIOR FILING DATE: 2000-09-26
PRIOR FILING DATE: 2000-09-26
PRIOR FILING DATE: 2000-09-26
PRIOR FILING DATE: 2000-09-27
PRIOR PRICATION NUMBER: US/60/235, 711
PRIOR PRILING DATE: 2000-09-27
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PRICE FILING DATE: 2000-09-18
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PRICE FILING DATE: 2000-09-20
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Best Local Similarity
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NUMBER OF SEQ ID NO
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APPLICANT: KOOPMAN, Peter Anthony
APPLICANT: MUSCAT, George Eugene Orlando
VIILE OF INVENTION: NOVEL POLYPEPTIDES AND POLYNUCLEOTIDES AND METHODS OF USING THEM
FILE REFERENCE: 21415-0003
CURRENT APPLICATION NUMBER: US/09/814,777A
CURRENT FILING DATE: 2001-03-23
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                            612 CCCTTGACGTCACCAGAAGGAGGTGCCGGGGTAGGAAGTGGGCTGGGGAAAGGTTATAAA 671
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                                                                                                                                                      672 TOSCOCCOGCOTOCGGOTGCTCCATCGAGGTCCGCGGAGGGTCGGAGGGCGCGCCAGGC 731
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US-05-814-777A-17
Science 17, Application US/09814777A
Patent No. US20020142415A1
GENERAL INFORMATION:
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PERIOR APPLICATION NUMBER: AU PQ6457
PRIOR FILING DATE: 2000-03-24

NUMBER OF SEQ ID NOS: 128
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CFHER INFORMATION: Intron NAME/KEY: misc_feature
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Best Local Similarity 48.09
Matches 179; Conservative
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OFHER INFORMATION: Exon
NAME/KEY: misc_feature
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CIHER INFORMATION: EXON
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CRGANISM: Human
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US-09-814-777A-17
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25418 CGCGCACGGCICCAAGGIGGIGGIGGCCGCCGTGGACGCGGIGAAAGCAICGACGAC 25477
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  Score 50.6; DB 10; Length 43658; Pred. No. 0.02; 0; Mismatches 255; Indels 2;
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Pred. No. 0.02;
0; Mismatches 255;
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Patent No. US20020142981A1
      5.4%;
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Similarity 46.69
28; Conservative
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SOFIWARE: Patentin Ver. 2.1
SEQ ID NO 3950
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Query Match
Best Local Similarity
Matches 228; Conserv
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US-09-880-107-3950
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TITLE OF INVENTION: Sets
FILE REFERENCE: 689290-76
                              15359 ACCCGGAGACCAAGACTACCGG-ACTTCGACCCGGGGGTCCGCGCAGTG 25417
                                                                                                            25418 CGCGCGCACGCTCCAAGGTGGTGGCCGCGTGGGCGGTGAAGAGCATCGACGAC 25477
                                                                                                                                                                                     25478 ATCGGGGCCCTGTCCAAGCTGAGCGGCCTACATCCTGCGGGGTGGACCG 25537
                                                                                                                                                                                                                                                              753 CCGGGAGGGGGGGGGGTCGGAGCGGGCTCGGGGTTCGGTGCAGGGGCCAAGGGGCG
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                                                                                 573 GAAGAGGTAGGTGGGGAGGCGGATGAGGGGTGGGGGACCCCTTGACGTCACCAGAAGGA 632
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PRIOR APPLICATION NUMBER: US/60/235,637
PRIOR APPLICATION NUMBER: US/60/235,638
PRIOR FILING DATE: 2000-09-26
PRIOR APPLICATION NUMBER: US/60/235,711
PRIOR APPLICATION NUMBER: US/60/235,720
PRIOR APPLICATION NUMBER: US/60/235,720
PRIOR FILING DATE: 2000-09-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION NUMBER: US/09/954,456
CURRENT FILING DATE: 2001-09-18
PRIOR APPLICATION NUMBER: US/60/233,617
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE: 2000-09-20
APPLICATION NUMBER: US/60/234,923
FILING DATE: 2000-09-25
APPLICATION NUMBER: US/60/235,134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR FILING DATE: 2000-09-18
PRIOR APPLICATION NUMBER: US/60/234,052
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PRIOR FILING DATE: 2000-09-27
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 529, Application US/09554456
Patent No. US20020115057AI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQ ID NOS: 2276
SOFTWARE: PatentIn version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2000-09-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION NUMBER: US/
PRIOR FILING DATE: 2000-09-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; ORGANISM: Homo sapiens
US-09-954-456-529
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            25778 GGTCGCGGG 25786
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
APPLICANT: Young, Paul
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    933 GCCGCGGG 941
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQ ID NO 529
LENGTH: 43058
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US-09-954-456-529
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7581 GGACGA 7576
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US-10-125-767-17/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Szalay, Aladar
TITLE OF INVENTION: ARTIFICIAL CHROMOSOMES, USES THEREOF
AND METHODS FOR PREPARING ARTIFICIAL THEOMOSOMES
25359 ACCGCAGACCAAGACCTACTTCCGC-ACTTCGACCTGCACCGGGGTCCGGCAGTTG 25417
                                                                                                                                                                                25418 CGCGCGCACGCCTCCAAGGTGGCCGCCGTGGGCGGGGGAAGGCATCGACGAC 25477
                                                                                                                                                                                                                                                 513 ACCCGCCTCGTCGGCCCCCCCCTCTCCGTAGCGCAAGCGAAGCGAGCCTGGGAGAA 572
                                                                                                                                                             693 CTICAICGAGGICCGCGGGAGGCICGGAGCGCCAGGCGGACACICCTCICGGCICCIC 752
                                                                                                                                                                                                                                                                                 753 CCCGGCCAGCGGCGCGCGCGCGCGCGCTCGGGGCTCGGGTGCAGCGGCCAGCGGGCG 812
                                                                                                                                                                                                                                                                                                                                                                                                     873 GCTCAGGGCGCGGCGGCGGCGGCGAACGAGGACGGACTCTGGCGGCCGGGTCTTT 932
                                                                                                  573 GAAGAGGTAAGTGGGGAGGCGGATGAGGGGTGGGGGACCCCTTGACGTCACCAGAAGGA
                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
ADDRESSEE: Heller Ehrman White & McAulliffe
STREET: 4250 Executive Square, 7th Floor
CITY: La Jolla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/09/799,462A FILING DATE: 10.Sep-2001 CLASSIFICATION: <UNKNOWN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: 08/835,682
FILING DATE: 10.APR-1997
APPLICATION NUMBER: 08/695,191
FILING DATE: 07.A0(1996
APPLICATION NUMBER: 08/682,080
FILING DATE: 15.JUL-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: 15-JUL 1996
APPLICATION NUMBER: 08/629,822
FILING DATE: 10-APR-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 1.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
NAME: Seldman, Stephanie L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 17, Application US/09799462A Patent No. US20020160970A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Hadlaczky, Gyula
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            USA
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US-09-799-462A-17/c
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389 GAGCCCGATGGGCAJJAGGAGGGCCAAGGGCAAGAGGCCGCGGAGCAAGACCCTGAACC 448
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           509 GGCCACCCGCCCTCJICGGCCCCCCCCTCTCCGTAGCCGCAGGGAAGCGAGCCTGGGA 568
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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Patent No. US20020160410A1
GENERAL INFORMATION:
APPLICANT: Hadlacky, Gyula
TITLE OF INVENTION: ARTIFICIAL CHROMOSOMES, USES THEREOF AND
                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                              Score 48.4; DB 9; Length 42999;
Pred. No. 0.059;
0; Mismatches 86; Indels 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ALDRESS:
ALDRESSEE: Heller Ehrman White & MCAULLÍFE LLP
STREET: 4350 La Jolla Village Drive, 7th Floor
REGISTRATION NUMBER: 33,779
REFERENCE/GACKET NUMBER: 24601-402G
IELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: Fast SEQ Version 1.5
CURRNY APPLICATION DATA:
APPLICATION WMBER: US/10/125,767
FILING DATE: 17-Apr-2002
PRIOR APPLICATION UMBER: 09/724,693
APPLICATION UMBER: 09/724,693
                                                                                                                                                                                                                                                                                     FRACHENT TYPE: «Gnknown»
ORIGINAL SOURCE:
SEQUENCE DESCRIFTION: SEQ ID NO: 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: 28-NOV-2000
APPLICATION WOMBER: 08/835,682
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DAIE: 10-APR-1997
APPLICATION NUMBER: 08/695,191
                                                                                                                                                    LENGTH: 42999 base pairs
                                                           TELEPHONE: 858-450-8403
TELEFAX: 858-587-5360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: ... COMPATIBLE OPERATING SYSTEM: DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE: 07-AUG-1996
                                                                                                                                                                                                                TOPOLOGY: linear
MOLECULE TYPE: Genomic DNA
                                                                                             TELEX: «Unxiown»
INFORMATION FOR SEQ 15 NO: 17:
SEQUENCE CHARACIERISTICS:
                                                                                                                                                                           TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ZIP: 92122
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                53.88;
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                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity 53.88 Marches 100; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CITY: San Diego
                                                                                                                                                                                                                                                        HYPOTHETICAL: NJ
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                                                                                                                                                                                                                                                                          ANTI-SENSE: NO
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673 GGCCCCCCCCCCCCTCGCTGTTCATCGAGGTCCGCGGAGGCTCGGAGCGCCCAGGCG 732
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Lees, Robert S.
APPLICANT: Lees, Simon W.
APPLICANT: Law, Simon W.
APPLICANT: Aljona, A.Ltal A.
TILLE OF INVENTION: WAVEL LOW DENSITY LIPOPROTEIN BINDING
TITLE OF INVENTION: PROTEINS AND THEIR USE IN DIAGNOSING AND TREATING
TITLE OF INVENTION: ATHEROSCIEROSIS
FILE REFERENCE: 107-0044001
CURRENT APPLICATION NUMBER: US/10/023,523
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      792 GGGTGCAGGGGCGCGCGGGGGGGGGGATTACCCGGGGAAGTGGTTGTCTCCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 47; DB 12; Length 2561;
Pred. No. 0.084;
                                                                                                                                                                                                                                              Score 47; DB 12; Length 25:
Pred. No. 0.084;
0; Mismatches 125; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               911 GGACICTGGCGGCCGGGTCTITGGCCGCGGG 941
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFIWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 48 LENGIH: 2561
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION NUMBER: US/09/616, 289
PRIOR FILING DATE: 2000-07-14
PRIOR PLING DATE: 2000-03-02
PRIOR PLING DATE: 2000-03-02
PRIOR PLING DATE: 157-11-26
PRIOR APPLICATION NUMBER: US 08/979, 608
PRIOR APPLICATION NUMBER: US 60/031, 930
PRIOR APPLICATION NUMBER: US 60/031, 930
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQ ID NOS: 5, SOFINARE: FASTSEQ for Windows Version 4.0 SEQ LENGTH: 2561
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION NUMBER: US 60/048,547 PRIOR FILING DATE: 1597-06-03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             . Sequence 48, Application US/10023523 ; Patent No. US20020152485A1
                                                                                                      ORGANISM: Oryctolagus cuniculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Oryctolagus cuniculus
                                                                                                                                                                                                                                              53.18;
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                                                                                                                                                                                                                                                                    Best Local Similarity 53.1 Matches 144. Conservative
                                                                                                                                               NAME/KEY: CDS
: LOCATION: (246)...(1895)
US-10-023-529-48
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LOCATION: (246)...(1895)
US-10-023-523-48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Lees, Ann M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-10-023-523-48/c
                                                                                  TYPE: DNA
                                                                                                                                                                                                                                                 Query Match
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                                                                                                                              FEATURE:
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APPLICANT: Lees, Robert S.
APPLICANT: Lees, Robert S.
APPLICANT: Law, Simon W.
APPLICANT: Law, Simon W.
APPLICANT: Law, Simon W.
TITLE OF INVENTION: APPLICANT AND THEIR USE IN DIAGNOSING AND TREAINS;
TITLE OF INVENTION: APPLICANTON APPROSCLEROSIS
FILE REFERENCE: 10797-004001
CURRENT APPLICATION NUMBER: US/10/023,529
CURRENT FILING DATE: 2001-12-17
PRIOR FILING DATE: 2000-07-14
PRIOR PELICATION NUMBER: US 09/515,849
PRIOR FILING DATE: 2000-03-12-26
PRIOR APPLICATION NUMBER: US 60/031,930
PRIOR PELING DATE: 1996-11-26
PRIOR APPLICATION NUMBER: US 60/031,930
PRIOR APPLICATION NUMBER: US 60/031,930
PRIOR APPLICATION NUMBER: US 60/031,930
PRIOR PELING DATE: 1996-11-27
PRIOR APPLICATION NUMBER: US 60/031,930
PRIOR PELING DATE: 1997-06-03
NUMBER OF SEQ ID NOS: 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             509 GGCCACCCGCCTCGTCGCCCCCCCCCTCTCCGTAGCCGCAGGGAAGCGAGCCTGGGA 568
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 5.1%; Score 48.4; DB 9; Length 42999; Best Local Similarity 53.8%; Pred. No. 0.059; Matches 100; Conservative 0; Mismatches 86; Indels 0;
                                                                                          AITORNEY/AGENT INFORMATION:
NAME: Sedidan, Stephanie L
REGISTRATION NUMBER: 33,779
REFERENCE/DOCKET NUMBER: 24601-402J
TELECOMMONICATION INFORMATION:
TELEPHONE: 858-450-8403
TELEPHAX: 858-587-5360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FRAGMENT TYPE: <Unknown>
SOUGHAL SOURCE:
GEOURICE DESCRIPTION: SEQ ID NO: 17:
US-10-125-767-17
APPLICATION NUMBER: 08/682,080
FILING DATE: 15-JUL-1996
APPLICATION NUMBER: 08/629,822
FILING DATE: 10-APR-1996
                                                                                                                                                                                                                                                                                                                            LENGTH: 42999 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 48, Application US/10023529
Parent No. US2002012388A1
GENERAL INFORMATION:
APPLICANT: Lees, Ann M.
                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear
MOLECULE TYPE: Genomic DNA
                                                                                                                                                                                                                                                      TELEX: «Unknown»
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                          HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ANTI-SENSE: NO
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464 CCCGGGCCCGCGTCGCCAGCACCTCCCCAGCGCGCTCGGCCCCGGGCCACCCGCCCTCG 523
         IIILE OF INVENTION: PROJEINS AND THEIR USE IN DIAGNOSING AND PREATING TITLE OF INVENTION: A.HEROSCLEROSIS FILE REFERENCE: 10797 -004001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   641 GGTAGGAAGTGGGCIJGGGAAAGGTTATAAATGGCCCCCGGCCTCGGCTGCTCTCATCG 700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 701 AGGICCGCGGGAGGCICGGAGCGCCCAGGCGGACACICCICTGGGCICCICCCCGGCAG 760
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CGGCGGCGCCTCGGARRGGGCTCCGGGCTCGGGTGCAGCGGCCAGCGGGCGCCTGGCGG 820
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      524 TCGGC--CCCCGCCCTCTCCGTAGCCGCAGGGAAGCGAGCCTGGGAAGAAGAAGAGGGT 581
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               821 CGAGGATTACCCGGGGAAGTGGTTGTCTCCTGGCTGGAGCCGCGAGACGGGCGCTCAGGG 880
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 45; DB 12; Length 1614;
Pred. No. 0.21;
0; Mismatches 230; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Lees, Ann K.
APPLICANT: Lees, Robert S.
APPLICANT: Law, Shon M.
APPLICANT: Law, Shon M.
APPLICANT: Arjona, Anibal A.
TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING
                                                                    CURRENT APPLICATION NUMBER: US/10/023,529
CURRENT FILING DATE: 2001-12-17
PRIOR PELICATION NUMBER: US/616,289
PRIOR FILING DATE: 2000-07-19
PRIOR FILING DATE: 2000-07-19
PRIOR FILING DATE: 2000-03-02
PRIOR PLING DATE: 1500-03-02
PRIOR PLING DATE: 1597-11-26
PRIOR APPLICATION NUMBER: US 60/031,930
PRIOR APPLICATION NUMBER: US 60/031,930
PRIOR APPLICATION NUMBER: US 60/031,930
PRIOR APPLICATION NUMBER: US 60/031,930
PRIOR APPLICATION NUMBER: US 60/031,930
PRIOR APPLICATION NUMBER: US 60/031,930
PRIOR APPLICATION NUMBER: US 60/031,930
PRIOR PRIOR DATE: 1957-10-60-03
                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQ ID NOS: 53
SOFIWARE: FastSEQ for Windows Version 4.0
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; Sequence 45, Applicatio; US/10023523
; Patent No. US2002015245541
; GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Homo sapiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ...(1614)
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: CDS
                                                                                                                                                                                                                                                                                                                                                                              SEQ ID NO 45
LENGIH: 1614
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; LOCATION: (1)
US-10-023-529-45
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FEATURE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                191
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                                                                      673 GECCCCCCCCCCTCGCTGCTTCATCGAGGTCCGGGGGGGTCCGGAGGCTCGGAGCGCCCAGGCG 732
                                                                                                                          733 -GACACTOCTOTOGGÉTOCTOCOCGGCAGOGGGGGGGCTOGGAGOGGGCTOCGGGGCTO 751
                                                                                                                                                                                                                                      705 CCGCGGGGAGGTCGGAGCGCGCCGAGCGGACACTCTTCGGCTCCTCCCCGGCAGGGGC 764
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      2; Gaps
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APPLICANT: Craig H. Day
APPLICANT: Craig H. Day
APPLICANT: Davin C. Dillon
APPLICANT: Mocowan, Partrick
APPLICANT: Sleath, Paul R.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DIAGNOSIS AND
INTLE OF INVENTION: TREATMENT OF HERPES SIMPLEX VIRUS INFECTION
FILE REFERENCE: 210121.538
CURRENT APPLICATION NUMBER: US/09/894,998
CURRENT FILING DATE: 2001-06-28
NUMBER OF SEQ ID NOS: 64
SOFTWARE: FastSEQ for Windows Version 4.0
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APPLICANT: Lees, Robert S.
APPLICANT: Law, Simon W.
APPLICANT: Law, Simon W.
APPLICANT: Arjona, Anibal A.
TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING
    Mismatches 125;
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55.6%; Pred. No. 0.11;
LVe 0; Mismatches 71;
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Patent No. US20020090610A1
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Patent No. US20020129388A1
GENERAL INFORMATION:
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Best Local Similarity 55.6%;
Matches 89; Conservative
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APPLICANT: Hosken, Nancy Ann
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US-09-894-998-35
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US-09-894-998-35/c
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Matches 144;
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RESULT 14
US-10-023-529-50/c
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TITLE OF INVENTION: PROTEINS AND THEIR USE IN DIAGNOSING AND TREATING TITLE OF INVENTION: ATHEROSCLEROSIS
FILE REPERENCE: 10797-004001
CURRENT APPLICATION WUMBER: US/10/023,523
CURRENT FILING DATE: 2001-12-17
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Pred. No. 0.21;
0; Mismatches 230; Indels
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Patent No. US20020147140a1
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REPERENCE: PC005
CURRENT APPLICATION NUMBER: US/09/764,877
CURRENT FILING DATE: 2001-01-17
                                                                              PRIOR APPLICATION NUMBER: US/09/616,289
PRIOR FILING DATE: 2000-07-14
PRIOR FILING DATE: 2000-07-14
PRIOR PELICATION NUMBER: US 09/517,849
PRIOR FILING DATE: 1097-11-26
PRIOR FILING DATE: 1997-11-26
PRIOR FILING DATE: 1997-11-26
PRIOR FILING DATE: 1996-11-27
PRIOR FILING DATE: 1996-11-27
PRIOR FILING DATE: 1996-11-27
PRIOR FILING DATE: 1997-06-03
NUMBER OF SEO ID NOS: 53
NUMBER OF SEO ID NOS: 53
SEQ ID NO 45
LENGTH: 1614
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Best Local Similarity 46.99
Matches 206; Conservative
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US-10-023-523-45
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GENERAL INFORMATION:
APPLICANT: Lees, Robert s.
APPLICANT: Lees, Robert s.
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APPLICANT: Lees, Robert s.
APPLICANT: Lees, Robert s.
APPLICANT: Lees, Robert s.
APPLICANT: Lees, Robert s.
APPLICANT: Lees, Robert s.
APPLICANT: Lees, Robert s.
APPLICANT: Arjona, Anibal A.
IIILE CF INVENTION: WORLE LOW DENSITY LIPOPROIEIN BINDING
IIILE CF INVENTION: AND THEIR USE IN DIAGNOSING AND TREATING
FILE REPERMED: 10797-004001
CURRENT APPLICATION NUMBER: US/01023,529
CURRENT FILING DAIE: 2001-12-17
FRIOR FILING DAIE: 2000-07-14
FRIOR FILING DAIE: 2000-07-14
FRIOR FILING DAIE: 1997-11-27
PRIOR FILING DAIE: 1997-11-27
PRIOR FILING DAIE: US 60/031,930
PRIOR APPLICATION NUMBER: US 60/031,930
                                                                                                                                                                                                                                                                              387 CIGAGCGCGAIGGGCAGGAGGAGGGCAAGGGCAAGAGGCGGGGGGGAGCAAAGACCCIGAA 446
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Prior application data removed - refer to PALM or file wrapper NUMBER OF SEQ ID NOS: 4031 SCTIMARE: Patentin Ver. 2.0 SEQ ID NO. 2718 LENGIH: 9566
                                                                                                                                                                                                    DB 10; Length 9968;
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Pred. No. 0.27;
0; Mismatches 270;
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. Patent No. US20020129386A1
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ilarity 45.8%;
Conservative (
                                                                                                       TYPE: DNA
CRGANISM: Homo sapiens
US-09-764-877-2718
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Best Local Similarity
Matches 232; Conserv
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Search completed: December 8, 2002, 14:44:53 Job time : 238.587 secs
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TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING
TITLE OF INVENTION: PROTEINS AND THEIR USE IN DIAGNOSING AND TREATING
TITLE OF INVENTION: ATHEROSCLEROSIS
FILE REFERENCE: 10797-004001
CURRENT APPLICATION NUMBER: US/10/023,523
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 12; Length 12425;
                                                                                                                                                                                                       Score 45, DB 12, Length 12.
Pred. No. 0.28;
0; Mismatches 230; Indels
                                      NUMBER OF SEQ ID NOS: 53
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION NUMBER: US/09/616, 289
RRIOR FILING DATE: 2000-07-14
PRIOR FILING DATE: 2000-03-02
PRIOR FILING DATE: 2000-03-02
PRIOR PAPLICATION NUMBER: US 08/579, 608
PRIOR PELING DATE: 1997-11.26
PRIOR APPLICATION NUMBER: US 60/031, 930
PRIOR FILING DATE: 1996-11-27
PRIOR FILING DATE: 1996-11-27
PRIOR FILING DATE: 1996-11-27
NUMBER OF SEQ ID NOS: 53
PRIOR APPLICATION NUMBER: US 60/048,547 PRIOR FILING DATE: 1997-06-03
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'atent No. US20020152485A1
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Matches 206; Conservative
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Law, Simon W.
                                                                                                                                     ORGANISM: Homo sapiens
US-10-023-529-50
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APPLICANT: Lees, Ann M.
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RS-10-023-523-50/c
                                                                                                      LENGTH: 12425
                                                                                                                         TYPE: DNA
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APPLICANT:
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                                                                                                                  DB 12; Length 12425;
                                                                                                              Score 45; DB 12; Length 124
Pred. No. 0.28;
0; Mismatches 230; Indels
    FastSEQ for Windows Version 4.0
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illarity 46.9%;
Conservative
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                                                 ; TYPE: DNA; ORGANISM: Homo sapiens
US-10-023-523-50
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Matches 206; Conserva
SOFTWARE: FastSE
SEQ ID NO 50
LENGIH: 12425
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/note= "Nucleotides numbered 1
through 1195 correspond to -1195 through -1 from
Figure 2."
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Sequence 1, Application US/0855424
Patent No. 5916/63
GENERAL INFORMATION:
APPLICANI: Williams, Lewis T.
APPLICANI: Wollshita, Kaoru
ITILE OF INVENTION: No. 5916/63al Promoter for VEGE Receptor
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 1745;
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SOFTMARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/556,424
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                   US-08-920-828613
US-08-804-1270-7
US-08-804-1286-11
US-08-945-958-7
US-09-430-854-7
US-09-949-125-49
US-09-940-125-49
US-09-810-964-49
US-08-810-270-11
US-09-810-270-11
US-09-811-24
US-09-913-011B-4
US-09-343-011B-4
US-09-343-011B-4
US-09-343-011B-4
US-09-343-011B-4
US-09-343-011B-4
US-08-343-011B-4
US-08-343-011B-4
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US-08-343-011B-4
US-08-757-6654-16
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  US-08-362-577C-13
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NAME: Dow, Karen B.
REGISTRATION NUMBER: 29,684
REFERENCE/DOCKET NUMBER: 2307K-063500US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-543-5043
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Townsend and Townsend and Crew
                                                                                                                                                                                                                                                                                                                                                                                                                   ALIGNMENTS
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
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INFORMATION FOR SEQ ID NO: 1:
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LENGTH: 1745 base pair:
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CITY. San Francisco
STATE: California
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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1 GCCGAAAAAGACACGGACAC......GCCGGGTCTTTGGCCGCGGG 941
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/cgn2_6/ptodata/1/ina/5B_COMB.seq:*
/cgn2_6/ptodata/1/ina/6A_COMB.seq:*
/cgn2_6/ptodata/1/ina/6B_COMB.seq:*
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               5.1.3
Compugen Ltd.
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US-08-483-533-36
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US-08-921-177-13
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                 Copyright (c) 1993 - 2002
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NUMBER OF INVENTION: NO NUMBER OF SEQUENCES: 1 CORRESPONDENCE ADDRESS: ADDRESS: Iownsend
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                                                           61 GIGCCAAGCAAGCGICAGIICCCCICAGGCGCICCAGGIICAGIGCCIIGIGCCGAGGGI 120
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US-09-263-914-1
Sequence 1, Application US/09263914
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APPLICANT: Williams, Lewis T. APPLICANT: Morishita, Kaoru

GENERAL INFORMATION: APPLICANT: Willian

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/note= "Nucleotides numbered 1
through 1155 correspond to -1155 through -1 from
Figure 2."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         241 ACCGICGCGGGGGCGGGGCCAGCIICCCTIGGAICGGACIIICCGGCCTAGGGCCAGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GGCGGAGCTICAGCCTIGTCCCTTCCCCAGTICGGGCGGCCCCCCAGAGCTGAGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ó;
6245512el Promoter for VEGF Receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 1745;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 100.0%; Pred. No. 1.6e-151;
Matches 941; Conservative 0; Mismatches 0;
                                                         Townsend and Crew
                                                                        Steuart Tower,
                                                                                                                                                                                              ULIMARE: PATENTIN PC-DOS/MS-DOS CURRENT APPLICATION DATA:
RAPILCATION NUMBER: US/04/7/7
FILING DATE:
                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/556,424
                                                                                                                                                                                   MEDIUM 1YPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                                                                                                                                 REGISTRATION NUMBER: 29,684
                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER: 23
TELECOMMUNICATION INFORMATION:
IELEPHONE: 415-543-9600
TELEPAX: 415-543-5043
                                                                        STREET: One Market Plaza,
CIIY: San Francisco
STAIE: Callfornia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INFORMATION FOR SEQ IL NO: 1;
                                                         and
                                                                                                                                                                                                                                                                                                                                                                                             ATHORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: misc_feature
ECCATION: 1..1195
 NO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACIERISTICS:
                                                                                                                                                                 CCMPUTER READABLE FORM;
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                 Dow, Karen 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IYFE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OTHER INFORMATION:
OTHER INFORMATION:
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750 TOGGGTGCAGCGGCCAGCGGCGCCTGGCGGAGGATTACCCGGGGAAGTGGTTGTCTC 849
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                                                                                                                                                                                                                                                          730 GCGGACACICCICTCGGCTCCICCCGGCAGCGGCGGCGGCTCGGAGCGGGCICCGGGGC 789
                                                                                                                                                                                                                                                                                Length 2313;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FOR INHIBITION OF
                                                                                                                                                                           Score 194.8; DB 1;
Pred. No. 3.7e-33;
0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: J. MARK HAND - MERCK & CO., STREET: 126 EAST LINCOLN AVENUE - P.O.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        179 CGGACTCTGGCGGCCGGGTCGTTGCCCGGGGG 210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            910 CGGACTCTGGCGGCCGGGTCTTTGGCCGCGGG 941
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: FastSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/427,353
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Sequence 1, Application US/09427353

Patent No. 6375529

GENERAL INFORMATION:

APPLICANT: THOMAS, KENNETH A.

APPLICANT: GOLDMAN, COREY K.

APPLICANT: KENDALL, RICHARD I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: BETT, ANDREW J.
APPLICANT: HUCKLE, WILLIAM R.
ITILE OF INVENTION: GENE THERAPY
TILLE OF INVENTION: ANGIGGENESIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REGISTRATION NUMBER: 36,545
REFERENCE/DOCKET NUMBER: 19:
FELECOMMUNICATION INFORMATION:
                                                                                                                                                                      Query Match
Best Local Similarity 98.1%;
Matches 208; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM Compatible OPERATING SYSTEM: DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE: ATTORNEY/AGENT INFORMATION:
                          LENGTH: 2313 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGIH: 2313 base pairs TYPE: nucleic acid
        SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: 732-594-4720
TELEX:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
                                                                                     TOPOLOGY: linear
HOLECULE TYPE: cDNA
US-08-232-538-5
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ZIP: 07065-0907
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CLASSIFICATION:
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                                                                                                                                            1160 AAGGTTATAAATCGCCCCCCCCCCCCCCCCCCCTCTTCATCGAGGTCCGCGGAGGCTCGGA 1219
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                                                                                                                                                                                                                             1220 GCGCGCCAGGCGACACTCTCTCGGCTCCCGCCGCGCGGCGGCGGCGCTCGGAGCGG 1275
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860 GGGTGGAGGAGTCTGCAAGGATTTCCTGAGCGCGATGGGCAGGAGGAGGGGCAAGGGCA 919
                                                                                                                        481 AGCACCTCCCCACGCGCGCTCGGCCCCGGGCCACCGCCCTCGTCGGCCCCCGCCCTCT 540
                                                                                                                                                                                                              600
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                                       421 AGAGGGCGCGGAGCAAAGCCTGAACCTGCCGGGCCGCGCTCCCGGGCCCGCGTCGCC 480
                                                             920 AGAGGGGGGGAGCAAAGACCCTGAACCTGCGGGGGCCGGCTCCCGGGGCCCGGGTCGCC
                                                                                                                                                                                                                                                                                                                                                                            AAGGTATAAAATGGCCCCGCCCTCGGCTGCTCTCATCGAGGTCCGGCGGGAGGCTCGGA
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                                                                                                                                                                                                          541 CCGTAGCCGCAGGGAAGCGAGCCTGGGAGGAGAAGAGGGGTAGGTGGGGAGGCGATGAG
                                                                                                                                                                                                                                                                                           601 GGGTGGGGGACCCCTTGACGTCACCAGAAGGAGGTGCCGGGGTAGGAAGTGGGCTGGGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                           GCGCGCCAGGCGGACACTCCTCGGCTCCTCCCGGCAGCGGCGGCGGCGCTCGGAGCGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Thomas, Kenneth A.
APPLICANT: Kendall, Richard L.
TITLE OF INVENTION: INHIBITOR OF VASCULAR ENDOTHELIAL CELL
TITLE OF INVENTION: GROWTH FACTOR
NUMBER OF SUGENECES:
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1400 ACGAGAGGACGGACCCGGGGTCTTTGGCCGCGGG 1440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           901 ACGAGAGGACTCTGGCGGCCGGGTCTTTGGCCGCGGG 941
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: Merck & Co., Inc.
STREET: P.O. Box 2000 126 E Lincoln Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/08/232,538
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NAME: Wallen, John W.III
REGISTRATION NUMBER: 35,403
REFERENCE/DOCKET NUMBER: 16888IA
TELECOMMUNICATION INFORMATION:
TELEPHONE: (908) 594-3905
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 5, Application US/08232538 Patent No. 5712380 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: (908) 594-4720 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY: USA
ZIP: 07065-0907
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STREET: F.C.
TTY: Rahway
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TELEFAX: 908-594-4720
TELEX:
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                                                                                                                                                       ORGANISM:
                                                                                                                                                                                                                                                                                                                                   Matches 208;
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                                                                                                                                                                                                                                                      US-09-051-363-1
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                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                            PEATURE:
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                                                                                                                                                                                                                                                                                                                                   790 TCGGGTGCAGCGCCCAGCGGCGCCTGGCGGCGAGGATTACCCGGGGAAGTGGTTGTCTC 849
                                                                                                                                                                                                                                                                                                                                                        61 TCGGGTGCAGCGGCCAGCGG--GCTGGCGGGGAGGATAACCCGGGGAAGTGGTTGTCTC 118
                                                                                                                                                                                                                                                                                                                                                                                                              850 CTGGCTGGAGCCGCGAGACGGGCGCTCAGGGCGCGGGGCCGGCGGCGGCGAACGAGGAGGA 509
                                                                                                                                                                                                                                                                                                                                                                                                                                       730 GCGGACACTCCTCTCGGCTCCTCCCCGGCAGCGCGGCTCGGAGCGGGCTCCGGGGC 785
                                                                                                                                                                                                                                                                           1 GGGGACACTCCTCTCGGCTCCTCCCGGCACGGCGGGGGGCTCGGAGCGGGCTCCGGGGC 60
                                                                                                                                                                          DB 4; Length 2313;
                                                                                                                                                                     Score 194.8; DB 4; Length
Pred. No. 3.7e-33;
0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Segawa, Toshiaki
TITLE OF INVENTION: VEGE-BINDING POLYPEPTIDES
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OPERATING SYSTEM: Windows95
SOFTWARE: FastSEQ for Windows Version 2.0
URRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/051,363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 179 CGGACTCTGGCGGCCGGGTCGTTGGCCGGGGG 210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            910 cGGACTCTGGCGGCCGGGTCTTTGGCCGCGGG, 941
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Fraser, Ph.D., J.D., Janis K. REGISTRATION NUMBER: 34,819
REFERENCE/DOCKEF NUMBER: 06501/012001
ELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/09/051,363
FILING DATE: 07-APR-1998
FARIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/JP96/02906
FILING DATE: 07-0CT-1996
APPLICATION NUMBER: 8/211892 JP
FILING DATE: 23-JUL-1996
APPLICATION NUMBER: 7/296476 JP
FILING DATE: 07-0CT-1996
APPLICATION NUMBER: 7/296476 JP
FILING DATE: 07-0CT-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: Fish & Richardson P.C. STREET: 225 Franklin Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-051-363-1; Sequence 1, Application US/09051363; Patent No. 6270993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
APPLICANT: Shibuya, Masabumi
APPLICANT: OKamoto, Masaji
APPLICANT: Niwa, Mikio
                                                                                                                                                                          20.7%;
98.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matsumoto, Tomoe
Asano, Makoto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IBM Compatible
                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Diskette
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Niwa, Mikio
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
    STRAIN---
TOPOLOGY: linear
NOLECULE TYPE: CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   02110-2804
                                                                                                                                                                                              Best Local Similarity
                                                     HYPOTHETICAL: NO ANTI-SENSE: NO FRAGMENT TYPE: CRIGINAL SOURCE: US-05-427-353-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEX: 200154
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                                                                                                                                                                                                                 208;
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STATE:
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                                                                                                                                                                                                                     Matches
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790 ICGGGIGCAGÓGGCCAGCGGCGCCTGGCGGCGAGGAITACCCGGGGAAGIGGIIGTCIC 849
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APPLICANT: KENDALL, RICHARD L
TITLE OF INVENTION: INHIBITOR OF VASCULAR ENDOTHELIAL
TITLE OF INVENTION: CELL GROWTH FACTOR
NUMBER OF SEQUENCES: 18
CCRRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 194.8; DB 4
Pred. No. 3.7e-33;
0; Mismatches 2;
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SIREET: P.O. Box 2000, 126 E. Lincoln Ave.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    175 CGGACICTGGCGGCCGGGTCGTTGCCCGGGG 210
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: 05/08/786,164
FILING DATE: 21-JAN-1997
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 5, Application US/08786164
Patent No. 5861484
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REFERENCE/DOCKET NUMBER: 18E
TELECOMMUNICATION INFORMATION:
IELEPHONE: 908-594-3905
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CELL TYPE: placental tissue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: Coding Sequence
LOCATION: 250...2523
INFCRMATION FOR SEQ ID NO: 1:
SEGUENCE CHARACTERISTICS:
LENGIH: 2523 base pairs
IYPE: nucleic acid
STRANDEDNESS: double
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ilarity 98.1%;
Conservative
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COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AIIORNEY/AGENT INFORMATION:
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PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
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SIRANDEDNESS:
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                         TOPOLOGY:
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                                                                                                                                                                                           Query Match
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                                                                                                                                                                                                                                                                                                            61 TCGGGTGCAGCGCCAGCGG--GCCTGGCGGCGAGGATTACCCGGGGAAGTGGTTGTCTC 118
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                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                        DB 2; Length 2651;
                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: MacLennan, David H
APPLICANT: O'Brien, Peter J.
TITLE OF INVENTION: DIAGNOSIS FOR PORCINE MALIGNANT
TITLE OF INVENTION: HYPERTHERMIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER REGARDELE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                  Query Match
20.7%; Score 194.8; DB 2;
Best Local Similarity 98.1%; Pred. No. 3.8e-33;
Matches 208; Conservative 0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 E: Bell, Seltzer, Park & Gibson
P.O. Drawer 34009
                                                                                                                                                                                                                                                                                                                                                                                                                            910 CGGACTCTGGCGCCGGGTCTTTGGCCGCGGG 941
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No. 6001976th Carolina 28234
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FILING DATE: 15-MAR-1993
ATTORNEY/AGENT INFORMATION:
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APPLICATION NUMBER: US/08/785,420
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Layton, Jr., Samuel G. REGISTRATION NUMBER: 22807
REFERENCE/DOCKET NUMBER: 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PELECOMMUNICATION INFORMATION:
INFORMATION FOR SEQ ID NO: 5: SEQUENCE CHARACTERISTICS: LENGTH: 2651 base pairs TYPE: nucleic acid STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEEX: 70-34-2014
TELEX: 77-5102
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
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nucleic acid
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APPLICATION NUMBER:
FILING DATE:
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CORRESPONDENCE ADDRESS
                                                                                                       CDNA
                                                                                     linear
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                                                                                  ; TOPOLOGY: lir
; MOLECULE TYPE:
US-08-786-164-5
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IIILE OF INVENIION: NOVEL BRAIN-SPECIFIC ADAPTER MOLECULE GENE
IIILE OF INVENIION: THEREOF, AND ANTIBODY THERETO
                                                                                                                                                                                                                         Score 55.4; DB 3; Length 15378;
Pred. No. 0.0017;
0; Mismatches 166; Indels 0;
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MEDIUM IYPE: Floppy disk
COMPUTER: IRM PC compatible
COMPUTER: IRM PC compatible
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DAIM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: PERRY, GLENN J.
REGISTRATION NUMBER: 28458
REPRENCE/DOCKET NUMBER: 7858/225548
RELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/08/729,416C
FILING DATE: 11-0CT-1996
CLASSIFICATION: 536
ATTORNEY AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 16, Application US/08729416C Patent No. 6013767 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               13232 AGAAGGTGACGGTGACCGAGC 13252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    863 CGAGACGGGGGCTCAGGGCGC 883
                                     DNA (genomic)
                                                                                                                                                                                                                         48.38;
                                                                                                                     CLONE: Porcine RYR1 Gene POSITION IN GENOME:
                                                                                                                                                                                                                                               Best Local Similarity 48.3
Matches 155; Conservative
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IELEX: 6714627 CUSH
single
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                 linear
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                                 MOLECULE TYPE:
                                                     HYPOIHETICAL:
ANTI-SENSE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLIFF 6.2313-0299
CCMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Tak PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOTIWARE: Patentin Release #1.0, Version #1.25
CURRINT APPLICATION DAPA:
APPLICATION NUMBER: US/08/232,463
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/935,313
FILING DATE:
APPLICATION NUMBER: EP 91 114 300.6
FILING DATE:
APPLICATION NUMBER: EP 91 114 300.6
FILING DATE: 26 AUG-1991
ATGNEST/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PACENT NO. 5670367
GENERAL INFORMATION:
APPLICANT: DORNER, F.
APPLICANT: SCHETELINGER, E.
APPLICANT: FALKNER, F. G.
TITLE OF INVANTION: RECOMBINANT FOWLPOX VIRUS
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAMS: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 30472/114 INMU
TELECHMUNICATION INFORMATION:
TELEPHONE: (703)836-9300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEE: Foley & Lardner: 1800 Diagonal Road, Suite 500 Alexandria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 14, Application US/08232463
Patent No. 5670367
                                                        TYFE: nucleic acid
STRANDEDNESS: double strand
TOPOLOGY: linear
INFORMATION FOR SEQ ID NO: 16. SEQUENCE CHARACTERISTICS: LENGTH: 1785 base pairs
                                                                                                                  ; MOLECULE TYPE: CDNA to mRNA
US-08-729-416C-16
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INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
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nucleic acid
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GENERAL INFORMATION:
APPLICAN: Xieff, Elliott D.
APPLICAN: Saleff, Elliott D.
APPLICAN: Salesas, Mary E.
APPLICAN: Ballesas, Mary E.
APPLICAN: RAPE, Kenneth M.
ITILE OF INVENTION: RHADINO VIRUS LANA ACTS IN TRANS ON A UNIT OF RHADINO ITILE OF INVENTION: VIRUS DNA TO MEDIATE EFFICIENT EPISCHE PERSISTENCE
TILE OF INVENTION: VIRUS DNA TO MEDIATE EFFICIENT EPISCHE PERSISTENCE
CURRENT ELLIGODALE: 1699-04-21
EARLIER APPLICATION NUMBER: US 60/109,422
FARIER APPLICATION NUMBER: US 60/109,422
FARIER FILINO DAIE: 1998-11-19
NUMBER C SEQ ID NOS: 3
SOFTWARE: PALENTIN Vér. 2.0
SEQ ID NO 3
LENGTH: 801
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   586 GGGGAGGCGGAIGAGGGGTGGGGGACCCCTTGACGTCACCAGAAGGAGGTGCCGGGGTAG 645
                                                                                                                                                                                                                          346 ASAGCIGAGIAAGCCGGGIGGAGGGAGICIGCAAGGATIICCIGAGGGGAIGGGCAAGA 405
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              218 COTCAGICCICCGIGCCAAGAACACGICGCGGAGGCGCGGCCAGGTICCCTIGGAICGG 277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         278 ACITICCGCCCNAGGGCGAGGCGGGGGGGGGTTCAGCCTTGICCCTTCCCCAGTTTCGGG 337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         338 CGGCCCCCAGAGCIGAGIAAGCCGGGIGGAGGGAGICIGCAAGGAIIICCIGAGCGCGAI 597
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      466 CGGGCCCGCGTCGCCAGCACCTCCCCACGCGCGCTCGGCCCCGGGCCACCCGGCCCTCGTC
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                                                                                                                                       DB 1; Length 7218;
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                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Mismatches 374; Indeis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           646 GAAGIGGGCIGGGGAAAGGTTATAAATCGCCCCCCCCCCTCGGC 688
                                                                                                                                  TYPE: DNA ORGANISM: Kaposi's sarcoma-associated herpesvirus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 3, Application US/09298568 Patent No. 6322792
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity 44.2 Matches 302; Conservative
SIRANDEDNESS: single
                                                                ; CLONE: PTZ9pt-F1s
US-08-232-463-14
                          linear
                       IOPOLOGY: line
IMMEDIATE SOURCE:
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US-09-298-568-3/c
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182 GÓCGCCGGCAGCGGCGGGGCGGGCAGCAGCAGCACCGGGCGCCCCCTGCGGGCG 541
                                        763 GOGGCGGCTCGGAGCGGGCTCCGGGGTGCAGCGGCCAGCGGGCGCCTGGCGGCG 822
                                                                823 AGGATTACCCGGGGAAGIGGIIGTCTCCTGGCTGGAGCCGCGAGACGGGGCGCTCAGGGCG
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                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Delcuve, Genevieve APPLICANT: Awang, Gregor IIILE OF INVENTION: Recombinant DNA Molecules and Expression TIILE OF INVENTION: Vectors for Itssue Plasminogen Activator
                                                                                                                                                                                                                 883 CGGGGCGCGCGCGAACGAGAACGACGAACTCTGGCGGCCG 925
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CCMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DCS/MS-DOS
SOFTMARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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27-JUN-1997
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US-08-683-795A-33/C
Sequence 33, Application US/08883795A
Patent No. 5885607
GENERAL INFORMATION:
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NAME: Gravelle, Micheline
REGISTRATION NUMBER: 46,261
REFERENCE/DOCKET NUMBER: 7841
IELECOMMUNICATION INFORMATION:
IELECOMMUNICATION (416) 364-7311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           E: Floppy disk
IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: BERESKIN & PARR STREET: 40 King Street West
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INFORMATION FOR SEQ ID NO: 3
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGIH: 3602 base pairs
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CORRESPONDENCE ADDRESS:
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MEDIUM TYPE: Floppy
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FILING DATE: 27-JUN
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Matches 122, Conserva
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21P: MS# 3Y2
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CIIY: Toronto
SIAIE: Ontario
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ORIGINAL SOURCE:
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SIRANDEDNESS:
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US-08+883-795A-33
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LOCATION:
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FEATURE:
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                398 GGGCAGGAGGAGGGCAAGGCCAAGAGGCCCGGAGCAAAGACCCTGAACCTGCCGGGC 457
                                                  578 GGGTAGGTGGGGAGGCGGATGAGGGGTGGGGGACCCCTTGACGTCACCAGAAGGAGGTGC 637
                                                                                                                                                                                                                                                                                                                                                                                                 698 TCGAGGTCCGCGGGAGGCTCGGAGCGCGCGGGGGCACACTCCTCGGCTCCTCCCCCGG 757
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                                                                                                                                                                                                                                                                                                                          Gaps
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APPLICANT: Tonlinson, James
APPLICANT: Tonlinson, CLOLING AND CHARACTERIZATION OF A HUMAN ADENYLYL
TITLE OF INVENTION: CLOLASE
TITLE OF INVENTION: CYCLASE
CURRENT APPLICATION NUMBER: US/09/473,716
CURRENT FILING DATE: 1999-12-29
PRIOR PELICATION NUMBER: CT/US/09/13540
PRIOR FILING DATE: 1999-07-01
PRIOR FILING DATE: 1997-07-01
                                                                                                                             518 CCCTCGTCGCCCCCCCCCCTCTCCGTAGCCGCAGGGAAGCGAAGCGAGGAAGAAGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            758 CAGCGGCGGCGCTCGGAGCGGGCTCCGGGCTGCAGCGGCCAGCGGCGCCTGG
                                                                                         CGCGCTCCCGGGCCCGCGTCGCCAGCACCTCCCCACGGGGGGGCTCGGCCCCGGGGCCACCCG
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Pred. No. 0.042;
0; Mismatches 109; Indels
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Patent No. 6436672
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     34 CGGTGTGGGGGGCGCGGGGCGCG 12
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Best Local Similarity 51.1%;
Matches 114; Conservative (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION NUMBER: 08
PRIOR FILING DATE: 1997-07-0
NUMBER OF SEQ ID NOS: 2
SOFTWARE: PALENTIN VEr. 2.0
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LOCATION: (139)..(3921)
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APPLICANT: TOMLINS
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SEQ ID NO 1
LENGTH: 4523
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US-09-473-716-1
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666 TATAAATCGCCCCCGCCCTCGGCTGCTTCAICGAGGTCCGGGGGGGGCTCGGAGCGGG 725
join(625..637, 1201..1346, 1605..1691, 2303..2482,
2617..2772)
                                                                                                       Length 3602;
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                                                                                                 5.1%; Score 48.2; DB 2; 149.8%; Pred. No. 0.05; tive 0; Mismatches 123;
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MEDIUM TYPE: Floppy disk
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                                                                                                                                                                                                                                                                                                                                          312/346-5750
                                                                                                                                                                                                                                                                                                                                                                                                                    1335 base pairs
                                                                                                                                                                                                                                                                                                                                                                       IELEX: 25-3856
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                CURRENT APPLICATION DAIA: APPLICATION NUMBER: PC
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                                                                                                                                                                                                                             19910910
                                                                                                                                                                                                                                                                                NAME: Gruber, Lewis S.
REGISTRATION NUMBER: 3
                                                                                                                                                                                                                                                                                                                                                       312/984-5740
   CURRESPONDENCE ADDRESS:
                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                   NUCLEIC ACTE
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                                                                             Illinois
                                                                                                                                                                                                                                 FILING DATE: 19
SLASSIFICATION:
                                             SIREET: Two Fi
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                                                                                                          60603
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                                                                                            COUNTRY:
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                                                                                                          644 TACTCACCGTGCACCCCCATCTCCGCGCCTGGCCGGGGTCCCTCAGCGACCTGGGGCGCG 585
                                              786 GGGCTCGGGTGCAGCGGCCCAGCGGGCCCTGGCGGCAGTTACCCGGGGAAGTGGTTG 845
                                                                                                                                                    APPLICANT: Sytkowski, Arthur J.

ITILE OF INVENTION: Production and Use of Recombinant
TITLE OF INVENTION: Protein Multimers With Altered Biological Activity
FILE REPRENCE: B1497-05A
CURRENT APPLICATION NUMBER: US/09/018,138
CURRENT FILING DATE: 1998-02-03
EARLIER APPLICATION NUMBER: 08/890,929
EARLIER PILING DATE: 1997-07-10
NUMBER OF SEQ ID NOS: 24
SCFWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              666 TATAAATCGCCCCCCCCCCTCGCTTCTTCATCGAGGTCCGCGGGAGGCTCGGAGCGCG 725
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 786 GGGCTGGGGGGGGCCAGGGGGGGGCGGGGGAGGATTACCCGGGGAAGTGGTTG 845
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0
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Vaccines and Methods:
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ECT-0591-06532-1/c

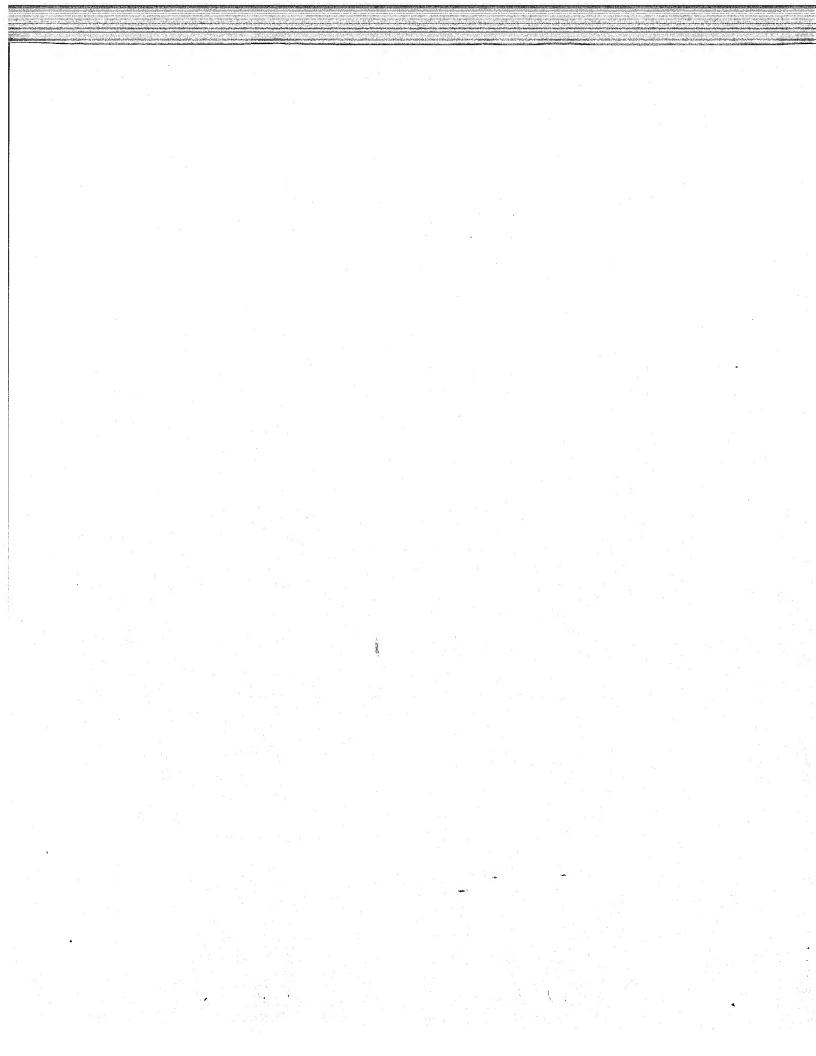
Sequence 1, Application PC/TUS9106532

GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                      09-018-138-1/c equence 1, Application US/09018138 Patent No. 6187564
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Roizman, Bernard
TITLE OF INVENTION: Recombir
TITLE OF INVENTION: Vaccines
NUMBER OF SEQUENÇES: 8
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Best Local Similarity
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                                                                                                                                                                                                               906 AGGAC 910
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Matches
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CCGAGGCACGGCCCGAIGACGCCTCGGCCACCGGCGCGCG-GAACGGAGCCG 808
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          417 GGCAAGAGGGGGGGAGCAAAGACCCIGAACCIGCGGGGCCGCGCTCCCGGGCCCGCGI 476
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      837 AAGIGGITGICICCISSCIGGAGCCGCGAGACGGGCGCTCAGGGCGGGGGGGCGGGCG 896
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  537 CICICCGIAGCGCAGGGAAGCGAGGCIGGGAGGAAGAAGAGGGIAGGTAGGAGGGA 596
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      597 IGAĞĞĞGIĞĞĞĞĞACCCTIĞACĞICACCAĞAAĞĞAĞĞIĞÇCĞĞĞĞIAĞĞAAĞIĞĞĞÇIĞ 656
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GGGAAAGGITATAAATCGCCCCCCCCCCTCGGCTGCTCTTCATCGAGGTCCGCGGGAGGCT 716
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      986 ACCGCTIGGIGCGGAGCICCCGGAAGICCGGGAAGACCCAGGCCGCCICGGGIGIAA 927
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46.0%; Pred. No. 0.067;
.lve 0; Mismatches 311; Indels 7
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray ADDRESSEE: Bicknell
                                                                                                                                                                                                                                                                                                 DPERALING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                             Two First National Plaza Suite 2100
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Pred. No. 0.085;
0; Mismatches 133; Indels 0
                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
ADDRESSEE: David A. Jackson, Esq.
STREET: 411 Hackensack Ave, Continental Plaza, 4th
897 GCGAACG----AGAGGACGGACTCTGGCGGCCCGGGTCTTTGGCCGCGG 940
                      TITLE OF INVENTION: CYCLIN-D BINDING FACTOR, AND USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPOTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET UNMER: 1340-1-002 N CP2
TELECOMUNICATION INFORMATION:
TELEPHONE: 201-487-5800
TELEFAX: 201-343-1684
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US/09/280,590A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: linear
MOLECULE TYPE: CDNA
HYPOTHETICAL: NO
ORIGINAL SOURCE:
ORANISM: Homo sapiens
SEQUENCE DESCRIPTION: SEQ ID NO: 36:
US-09-280-590A-36
                                                                                                                                         Sequence 36, Application US/09280590A; Patent No. 6303772
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: 29-Mar-1999 CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ZIP: 07601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 5703 base pairs TYPE: nucleic acid STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY AGENT INFORMATION:
                                                                                                                                                                                                                                                      Inoue, Kazushi
Bodner, Sarah M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION DATA:
                                                                                                                                                                                                            APPLICANT: Hirai, Hiroshi
Sherr, Charles
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO: 36:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 5.0%;
Best Local Similarity 48.8%;
Matches 127; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STATE: New Jersey
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                              CITY: Hackensack
                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                            Floor
                                                                                                                         US-09-280-590A-36
                                                                                                          RESULT 15
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Soluble VEGF recep Human VEGF recepto cDNA encoding amin Human soluble vasc

soluble VEGF

transductio

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Oligonucleotide fo Oligonucleotide fo MH mutant porcine Human colon cancer

Human colon cancer Human colon cancer

herpesvirus herpesvirus

Human Human

ABQ52496

AAD25519 AB052497

Human adenosine Al gene express

DNA encoding novel Flt-lextraFAStm/cy

SVEGF-RI gene.

AAQ74268 AAS70286

AV01457

\AA91131 AAX53491

4AX53491

Human colon cancer

AA02539

ABQ40801

ABQ4345 AAA3029 ABN9745

AAA02484

Rat brain-specific

Oligonucleotide fo Oligonucleotide fo

Nucleotide sequenc Kaposi's sarcoma-a

Rhadino virus cis-Gene #3953 used to

fo fo

Oligonucleotide Oligonucleotide

Lung cancer relate Lung cancer relate

Rianodin receptor

ALIGNMENTS

AAQ10613

trafficking;

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Flt-1; VEGF receptor; vascular endothelial growth factor; human; vascular permeability factor; fms-like receptor tyrosine kinase; hypertension; thromicsis; atherosclerosis; restenosis;
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Jabel- els
Anote- *E26 transformation specific sequence*
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/note=" m226 transformation specific sequence"
1098..1103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Inflammatory disease; haemophilia; wound healing; diabetic retinopathy, rheumatoid arthritis; blood cell tratumour; angiogenesis; gene therapy; transgenic animal; ss
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/note= "(claim 4)"
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Human gene regulat
Signal transductio
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Promoter of human
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Chemically treated
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                                                                                                                                  (without alignments)
[1193.756 Million cell updates/sec
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                                                                                                              8, 2002, 07:50:37; Search time 189.314 Seconds
                                                                                                                                                                              /SIDS2/gcgdata/geneseg/genesegn-embl/NA2001A.DAT:*/SIDS2/gcgdata/geneseg/genesegn-embl/NA2001B.DAT:*
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /SIDS2/gcgdata/geneseq/geneseqn.embl/NA1989.DAI:*/SIDS2/gcgdata/geneseq/geneseqn.embl/NA1990.DAI:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /SIDS2/gcgdata/geneseq/geneseqn.embl/NA1991.bAT;*/SIDS2/gcgdata/geneseq/geneseqn.embl/NA1992.bAT;*/SIDS2/gcgdata/geneseq/geneseqn.embl/NA1993.bAT;*
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1996.DAT:*/SIDS2/gcgdata/geneseq/geneseqn-embl/NA1997.DAT:*
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/SIDS2/gogdata/geneseq/geneseqn-embl/NN1988.DAT:
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                                                                                                                                                                                                                                                                                                                                    4370478
               GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd:
                                                                                                                                                                                                                                                                                                                                tal number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                               2185239 seqs, 1125999159 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Listing first 45 summaries
                                                                               OM nucleic - nucleic search, using sw model
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AA$46351
ABL70215
AA$61170
ABK31260
ABQ67063
AA$46352
ABL70216
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                                                                                                                                                                                                                                                 IDENTITY_NUC Gapop 10.0 , Gapext 1.0
                                                                                                                                                                                                                                                                                                                                                                                                                 Post-processing: Minimum Match 0% Maximum Match 100%
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                                                                                                                                                                                                                                                                                                                                                                inimum DB seq length: 0 ximum DB seq length: 20000000000
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                                                                                                                  December
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from the mammal, selecting cells which have incorporated and express the gene and reimplanting them into the mammal (claimed). The transgenic or chimeric animal can be used as a disease model. Of as a bloreactor for the production of large amounts of protein.

3538888888XX

Sequence 1745 BP; 315 A; 501 C; 621 G; 308 I; 0 other;

or antisense RNA, which reduces vascular permeability or has antimitogenic activity, operably liked to the VEOF receptor promoter, it can be used to inhibit tumour anglogenesis following the incroduction into the endothelial cells links the tumour, or control anglogenesis in a mammal by transfecting cells explanted

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/*tag= d
/note= "forms separated palindrome with bases 1109-
1114"
                                                           separated palindrome with bases 1098-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Vascular endothelial growth factor receptor promoter · useful to develop products to treat, e.g. tumours, hypertension, thrombosis, atherosclerosis or inflammatory diseases
                                                                                                                       "cAMP response element binding protein/
activated transcription factor"
                                                                                                                                                                                     transformation specific sequence"
                                                                                                                                                                                                                                     transformation specific sequence"
                                                                                                                                                                                                                                                                                                                                                                                                /*tag= m
/note= "transcription arrest site"
                                                                                                                                                                                                                                                                                               transcription start site
                                                                                                                                                                                                                                                                                                                                                                     /note= "5' portion of intron 1"
1602..1621
                                                                                                              CAEB/ATF
                                                                                                                                                                                                                                                                                                                                 'note- "exon 1"
                                         /*tag= e
/note= "forms s
/note= 1103"
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/note- "E26 t
1157..1160
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  Score 941; DB 18; Length 1745; Pred. No. 1.4e-175;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             hypertension, thrombosis, atherosclerosis, restenosis, inflammatory diseases, haemophilia, wound healing, diabetic retinopathy, rheumatoid arthritis and blood cell trafficking. When it further
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   comprises a gene encoding a protein, polypeptide, hormone, ribozyme
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Claim 4; Fig 2A-B; 70pp; English.

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                                                                                 ALS47815 LII_NFL006_PL2 Homo sapiens CDNA clone CS0D1033YD17 5
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Engaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammala; Eutheria; Primates; Catarrhini; Hominidae; Homo.
11. (bases 1 to 1002)
11. W.B., Gruber, C., Jessee, J. and Polayes, D.
Full-length CDNA libraries and normalization
Contact; Genoscope
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BP 191 91006 EVRY cedex - France
Email: segref@genoscope.cns.fr, Web : www.genoscope.cns.fr.
Location/Qualifiers
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/db_xref="taxon:9606"
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//issue_type=foliacenta*
//orce_vvector: pCWYSPORT 6; Site_l: Not!; lst strand CDNA,
//orce_vvector: pCWYSPORT 6; Site_l: Not!; lst strand CDNA,
was primed with a NotTooligo(d) primer. Five prime end
enriched with a NotTooligo(d) primer. Five prime end
enriched, double-stranded CDNA was digested with Not I and
Cloned into the Not I and Eco RV sites of the pCMYSPORT 6
vector. Library was normalized. Library was constructed by
life lechnologies. Contact : Feng Liang Life Technologies.
a division of Invitrogen 8800 Medical Center Drive
Rockville, Maryland 20850, USA Fax : (1) 301 510 8371
Email : fliangelifetech.com URL :
http://fulllength.invitrogen.com*
character.
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                            61 GCGGCCCCGGGGCTCGGGTGCAGCGGCCAGCGGGCCCTGGCGCGAGCATTACCCGGG 120
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Location/Qualifiers
1. .972
776 GCGGGCICCGGGGCICGGGIGCAGCGGCCAGCGGGCGCCIGGCGGGGGGGAIIACCCGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Eutele
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
1 (bases 1 to 972)
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/db_xref="taxon:9606"
/clone="CSODIOO2x109"
/clone_lib="LTI_NFL006_PL2"
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1025)
                                                                                                                                                                                                                                  Email: genomicsfhri.co.jp
HRI human cDNA project; 5'- & 3' end one pass sequencing: Helix
Research Institute; cDNA library construction: Department of
Virology, Institute of Medical Science, University of Tokyo, and
Helix Research Institute.
                                     Ota,T., Nishikawa,T., Suzuki,Y., Ishii,S., Saito,K., Rawai,Y., Yamamoto,J., Wakamatsu,A., Nakamura,Y., Nagai,T., Sugano.S. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            721 GCGCCCAGGCGSACACTCCTCGGCTCCTCCCCGGCAGGGCGCGCGCTCGGAGGGG 780
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Location/Qualifiers
Manmalia: Eutheria: Primates: Catarrhini; Hominidae: Homo.
1 (bases 1 to 652)
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Live 0; Mismatches 5; Indels 0
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                                                                                                                                                                                 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
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/clone_lib="PLACEI"
/lissue_type="Placenta"
/note="Vector: pME188EE13"
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/db_xref="taxon:9506"
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                                                                                                                                                                Helix Research Institute
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                                                                                           HRI human cDNA project
                                                                                                            Unpublished (2000)
Contact: Takao Isogai
Genomics Laboratory
                                                                                                                                                                                                  Tel: 81-438-52-3975
Fax: 81-438-52-3986
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Best Local Similarity 97.77
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/note="vector: provided in the strand country is strand country was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-stranded cDNA was digested with Not I and cloned into the Not I and Eco RV sites of the powNSPORI 6 vector. Library was normalized. Library was constructed by Life Technologies. Contact: Feng Liang Life Technologies, a division of Invitrogen 9800 Medical Center Drive Rockville, Maryland 20850, USA Fax: (1) 301 510 8371 Email: filang@lifetech.com URL.

Examil: filang@lifetech.com URL.
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Manmalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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/clone="CSODIO61YO18"
/clone_lib="LII_NFL006_PL2"
/tissue_type="placenta"
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//tissue_type="placenta"
//tissue_type="pla
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Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                Email: segref@genoscope.cns.fr, Web : www.genoscope.cns.fr
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Pred. No. 3.6e-30;
                                                                                                                                        Length 638;
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Full-length cDNA libraries and normalization
Unpublished (2001)
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BP 191 91006 EVRY cedex - France
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                                                                                                                                      DB 9:
Email : fliang@lifetech.com URL
                                                                                                                                Score 211.4; DB 9
Pred. No. 6.2e-31;
                                                                                                                                                         Pred. No. 6.2e
0; Mismatches
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/clone="CS0DI030YL03"
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/note-Torgon Pancreas; Vector: pBluescript SK(-): Site_1:
Noti's Site_2: Xho; cDNA made by oligo-dT priming.
Size-selected on agaross gel. Average insert size -1kb. 5'
XhoI site was destroyed affer directional cloning.
Amplified once. Contact information: Hiroshi inoue, MD,
Metabolism Div. (Alan Permutt Lab), Washington University
School of Medicine, Box 8127, 660 South Buclid Ave., St.
Ilouis, MO 63110, E-mail: hinoue@imgate.wustl.edu, Tel:
314-382-1916, Fax: 314-747-2692."
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Fukayota: Metazoa: Chordata; Craniata; Vertebrata; Euteleostomi;
Fukayota: Metazoa: Chordata; Catarrhini; Hominidae: Homo.
1 (bases 1 to 584)
Melton.D., Brown.J., Kenty.G., Permutt.A., Lee,C., Kaestner.K.,
Lemiskhai., Scearce.M., Pape.D., Wylie.T., Martin.J., Blistain.A.,
Schmitt.A., Theising.B., Ritter.E., Ronko.I., Bennett.J., Cardenas,
M., Gibbons,M., McCann.R., Cole,R., IsagarāishVili.R., Williams.T.
Endocrine Pancreas Consortium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Harvard University, Howard Hughes Medical Institute
Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge,
MA 02138
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606
                                                                                                                        ikl4007.yl HR85 islet Homo sapiens CDNA clone IMAGE: 5780553 Similar to TR:012954 012954 SOLUBLE VASCULAR ENDOTHELIAL CELL GROWTH FACTOR RECEPTOR. ;, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Unpublished (2000).
Other_ESTs: ikl4a07.xl
Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue
                                                                                    850 CTGGCTGGAGCGGCGAGACGGGCGCTCAGGGCGGGGGGGCCGGCGGCGGCGGCGAACGAGGGA
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Pred. No. 5.2e-30;
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/tissue_type="Purified pancreatic islet"
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/db_xref="taxon:9606"
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High quality sequence stop: 476.
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Email: dmelton@biohp.harvard.edu
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BQ271447.1- GI:20496513
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LOCUS ALS40382 B67 bp mRNA linear EST 16-FEB-2001 DEFINITIN ALS40382 LII_FL002_PL1 Homo sapiens cDNA clone CS0DE001KK21 5 prime, mRNA sequence.
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                                                                                                                                                                                                    AL549158 AL549158 I.II_NFL006_FL2 Home sapiens CDNA clone CS0DI051XP21 5
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Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
Full-length; cDNA libraries and normalization
Unpublished (2001)
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Genoscope - Centre National de Sequencage
BP 191 91006 EVRI cedex - France
Email: segref@genoscope.cns.fr, Web : www.genoscope.cns.fr.
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/db_xref="taxon:9606"
/clone="CSOD1051YP1"
/clone=lib="III="IIIINFL006"
/tissue_type="placenta"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ü
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 CCGGGGCTCGGGTGCAGCGGCCAGCGGNGCGCCTGGCGGGGGGGAGGATACCCGGGGAAGTG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               842 GIIGICICCIGGCIGGAGCCGCGACACGGCCCICAGGCGCGCGGGCCGCGGCGGCGAA 901
                                              729 GGCGGACACICCTCICGGCICCTCCCCGGCAGCGGCGGCGGCTCGGAGCGGGCTCCGGGG 788
                                                                                                                                                             849 CCTGGCTGGAGCCGCGAGACGGGCGCTCAGGGCGCGGGGCGGCGGCGGCGGCGGCGAACGAGGAGG 908
                                                                                                                                                                                                                                                                           121 CCIGGCIGGAGCCGCGAGACGGCCCICAGGCCGCGGGGCCGGCGGCGGCGAACGAGGGG 180
                                                                                                                                     CICGGGIGCAGCGGCCAGCGGGCGCCIGGCGGCGAGGAIIACCCCGGGGAAGIGGIIGICI 848
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    Gaps
                                                                                         1 GGCGGACACTCCTCTCGGCTCCTCTCTGCACCGGCGGCGCTCGGAGCGGGCTCCGGGG 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: segref@genoscope.cns.fr, Web : www.genoscope.cns.fr.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           723 GCGCCAGGCGGACACICCICICCGCCTCCCCCCGGCAGCGGCGGCGGCGGCTCGGAGCGGGCT
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  Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: fliang@lifetech.com URL:
http://fulllength.invitrogen.com"
267 c. 272 g 209 t
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BP 191 91005 EVRY cedex - France
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /clone_lib="LTI_NFL006_PL2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Mismatches
  Mismatches
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/db_xref="taxon:9606"
/clone="CSODIO06YF20"
  0;
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  Conservative
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Best Local Similarity
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ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM
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TITLE
JOURNAL
    Matches
                                                                                                                                     789
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KEYWORDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMMENT
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pcMvSFORI 6 vector. Library was constructed by Life Technologies. Contact: Feng Liang Life Technologies, a division of Invitrogen 9800 Medical Center Drive Rockville 1 Maryland 20850, USA Fax: (1) 301 610 8371 Email: Http://fulllength.invitrogen.com*

226 c 250 g 170 t 2 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="Organ: placenta; Vector: pCMVSPORT 6; 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-stranded cDNA was digested with Not I and cloned into the Not I and Eco RV sites of the pCMVSPORT 6 vector. Library was constructed by Life
                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 857)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       716 TCGGAGCGCGCCAGCCGGCACACTCCTCGGCTCCTCCCCGGCAGCG-CCGCGGCTCGG 774
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        834 GCCAAGTGGTTGTCTCCTGCTGGAGCCGCGAGACGGGCCCTCAGGGCCGCGGGCCGCCG
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BP 191 91005 EVRY cedex - France
Email: segref@genoscope.cns.fr, Web : www.genoscope.cns.fr.
Location/Qualifiers
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Pred. No. 3.9e-29;
1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     894 GCGCCGAACGAGGACGGACTCTGGCCGGGTCTTTGGCCGCGGG 941
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                                                                                                                                                                              Liw.B., Gruber.C., Jessee,J. and Polayes,D. Full-length cDNA libraries and normalization Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                             /organism="Homo sapiens"
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/clone="CSODE001XX21"
/clone_lib="LII_EL002_PL1"
/lab_host="DH10B"
                       AL540382.1 GI:12870475
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Best Local Similarity 98.2%;
Matches 224; Conservative
                                                                                                                                                                                                                                              Contact: Genoscope
                                                                                                                                                                                                                                                                                                                                                          1. .867
                                                                                           Homo sapiens
                                                                      human.
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ORIGIN
                     VERSION
KEYWORDS
SOURCE
CRGANISM
                                                                                                                                                                                                     TITLE
JOURNAL
COMMENT
                                                                                                                                                         REFERENCE
AUTBORS
ACCESSION
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Search completed: December 8, 2002, 12:49:39
Job time: 1237.21 secs

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3395 CCCGACTCCCTITGAAGTGGATGGCCCCGGAACCATTTTGACAGAGTATACACAATTC 3454
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            24.8%; Score 74.6; DB 1; Length 5406; 78.8%; Pred. No. 4.1e-14; Live 0; Mismatches 24; Indels 0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Lemischka, Ihor R.
IIILE OF INVENTION: TOTIPOTENT HEMATOPOIETIC STEM CELL
IIILE OF INVENTION: RECEPTORS AND THEIR LIGANDS
WUMBER OF SEQUENCES: 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
COMPUTER: PC-DOS/MS-DOS
SOFTWARE: Petentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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PRIOR APPLICATION DATA: 15-AFR-1992
APPLICATION NUMBER: US PCT/US92/02750
FILING DATE: 02-APR-1992
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: IMClone Systems Incorporated STREET: 180 Variok Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          us PCI/US92/05401
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CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US UNASSIGNED FILING DATE: 12-NOV-1992
RADE APPLICATION NUMBER: US 07/906,397
FILING DATE: 26-JUN-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US/07/977,451
FILING DATE: 19521119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 5, Application US/07977451
Patent No. 5270458
GENERAL INFORMATION:
REFERENCE/DOCKET NUMBER: LE TELECOMMUNICATION INFORMATION: TELEPHONE: 212-645-1405 IELEERX: 212-645-2054 INFORMATION FOR SEQ ID NO: 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: 26-JUN-1992
PRIOR APPLICATION DATA:
                                                                                                        SEQUENCE CHARACTERISTICS:
LENGTH: 5406 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: SLigle
                                                                                                                                                                                                                                                                                                                                                                                                                                                   89; Conservative
                                                                                                                                                                                                                                                                                                                        mat_peptide
208..4308
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                                                                                                                                                                                                                                                                              208..4311
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                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
                                                                                                                                                                                                                    MOLECULE TYPE: CDNA
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SIATE: New York
COUNTRY: U.S.A.
ZIP: 10014
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                                                                                                                                                                                                                                                              NAME/KEY:
                                                                                                                                                                                                                                                                                LOCATION:
                                                                                                                                                                                                                                                                                                                        NAME/KEY:
                                                                                                                                                                                                  TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                            ; LOCATION:
US-07-813-593-3
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US-07-977-451-5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 76.2; DB 2; Length 4236; Pred. No. 1.1e-14; 0; Mismatches 23; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: TOTIPOTENT HEMATOPOIETIC STEM CELL TITLE OF INVENTION: RECEPTORS AND THEIR LIGANDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OCHANTIA SYSTEM: PC-OSS/MS-DOS
OCHANTE: PATENTIA RELEASE #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/815,593
FILING DATE: 19920415
CLASSIFICATION NATA:
APPLICATION NUMBER: US 07/793,065
FILING DATE: 15-NOV-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/728,513
FILING DATE: 28-JUN-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/679,665
FILING DATE: 20-JUN-1991
ATORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: IMCLONE SYSTEMS INCORPORATED
STREET: 180 VARICK STREET
                        APPLICATION NUMBER: US/07/930,548A FILING DATE: 23-NOV-1992 CLASSIFICATION: 435
                                                                                                                                                       31,298-01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 3, Application US/07813593 Patent No. 5185438 GENERAL INFORMATION:
                                                                                                                                              REFERENCE/DOCKET NUMBER: 31,2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-831-3344
TELEFAX: 201-831-3305
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Lemischka, Ihor R.
                                                                                                                                   30,637
                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: DNA (genomic)
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79.6%;
                                                                                         ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                    LENGIH: 4236 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 79.64
Matches 90; Conservative
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        CURRENT APPLICATION DATA:
                                                                                                                 NAME: Gordon, Alan M. REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                      TYPE: nucleic acid
STRANDEDNESS: single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CITY: NEW YORK
STATE: NEW YORK
COUNTRY: U.S.A.
ZIP: 10014
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                                                                                                                                                                                                                                                                                                                                                                                                                               LOCATION:
US-07-930-548A-7
                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY:
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3355 CCCGACTCCCTTTGAAGTGGATGGCCCGGAAACCATTTTTGACAGAGTATACACAATC 3454
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       24.8%; Score 74.6; DB 1; Length 5406; 78.8%; Pred. No. 4.1e-14; Live 0; Mismatches 24; Indels 0
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Patent No. 5548065
GENERAL INFORMATION:
APPLICANT: Lemischka, Thor R.
ATILE OF INVENTION: TOTIPOTENT HEMATOPOLETIC STEM CELL.
ITILE OF INVENTION: RECEPTORS AND THEIR LIGANDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATINS SYSTEM: PC-DOS/MS-DOS
OFTRARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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CORRESPONDENCE ADDRESS:
ADDRESSE: Inclone Systems Incorporated
SIREET: 180 Varick Street
CIIY: New York
                                    FILING DAIE: 05/01/340.000
FILING DAIE: 05/01/340.000
CLASSIFICATION: 536
PRIOR APPLICATION BAIN
FRING APPLICATION BAIN
FRING APPLICATION DAIN:
FRING APPLICATION ADMER: 05/07/93,065
FILING DAIE: 15-NOV-1991
PRIOR APPLICATION DAIN:
FILING DAIE: 15-NOV-1991
PRIOR APPLICATION NUMBER: 05/07/28,913
FILING DAIE: 28-JUN-1991
FRIOR APPLICATION NUMBER: 05/07/728,913
FILING DAIE: 28-JUN-1991
APPLICATION NUMBER: 05/07/728,913
FILING LAIE: 02-APR-1991
APPLICATION NUMBER: 05/07/728,913
FILING LAIE: 02-APR-1991
                                                                                                                                                                                                                                                                                                                                                                                        NAME: Felt, Irving N.
AEGISTRAITON NUMBER: 28,601
REFERRNCE/DOCKET NUMBER: LEM-3-PPP
IELECHMUNICATION INFORMATION:
IELEPHONE: 212-645-1405
IELEFAX: 212-645-2054
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGIH: 5406 base pairs
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Matches 89; Conservative
    URRENT APPLICATION DATA:
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208..4308
                          APPLICATION NUMBER: US
FILING DATE: 19920917
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MOLECULE TYPE:
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FEATURE:
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; LOCATION:
US-07-946-507-3
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NAME/KEY:
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US-08-252-517-5
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TITLE OF INVENTION: TOTIPOTENT HEMATOPOIETIC STEM CELL
TITLE OF INVENTION: RECEPTORS AND THEIR LIGANDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
CERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: IMCLONE SYSTEMS INCORPORATED STREET: 180 VARICK STREET
                                                                                                       PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 07/728,913
FILING DATE: 28-40n-1991
PRIOR APPLICATION NUMBER: US 07/679,666
FILING DATE: 02-APR-1991
ATOMENY/AGENT INFORMATION:
NAME: Felt, Irving N.
REGISTRATION NUMBER: LEM-3-7P
TELEPHONE: 212-645-1405
TELEPHONE: 212-645-1405
APPLICATION NUMBER: US 07/813,593
FILING DATE: 24-DEC-1991
PRIOR APPLICATION DATA:
                                                                   UMBER: US 07/793,065
15-NOV-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-07-946-507-3; Sequence 3, Application US/07946507; Patent No. 5283354
                                                                                                                                                                                                                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO: 5: SEQUENCE CHARACTERISTICS: LENGTH: 5406 base pairs TYPE: NUCLEIC ACID STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FRAGMENT TYPE: N-terminal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
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265..4308
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208..264
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
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                                                                        APPLICATION NUMBER: FILING DATE: 15-NOV
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MOLECULE TYPE: CDNP
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity
Matches 89; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
APPLICANT: Lemisch
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ZIP: 10014
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LOCATION:
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US-07-977-451-5
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U.S.A.

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Sequence 5, Application US/07906397A
Patent No. 5521090
GENERAL INFORMATION:
APPLICAM: Lemischka, Ihor R.
TILLE OF INVENTION: TOTIPOTENT HEMATOPOIETIC STEM CELL
TILLE OF INVENTION: RECEPTORS AND THEIR LIGANDS
                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/07/906,397A ELING DATE: 19920626 CLASSIFICATION S36 PHUG APPLICATION DATA:
                                                                                                                                                CCKEES: ONDERESS: ADDRESS: ADDRESS: ADDRESSEE: IMCLONE SYSTEMS INCORPORATED SIREET: 180 VARICK SIREET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REJISTRATION NUMBER: 28,601
REFERENCE/DOCKET NUMBER: LEM-3-PPPPPP IELECCHANNICATION INFORMATION:
IELEPHONE: 212-645-1405
IELEFAX: 212-645-2054
INFORMATION FOR SEQ ID NO: 5:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US 07/793,065
FILING DATE: 15-NOV-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/728,913
FILING DATE: 28-JUN-1991
PRIOR APPLICATION NUMBER: US 07/679,666
FILING DATE: US 07/679,666
FILING DATE: US APPLICATION NUMBER: US 07/679,666
FILING DATE: US APPR-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US 07/813,593 FILING DATE: 24-DEC-1991
PRICR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                              MEDIUM IYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                ZIP: 10014
COMPUIER READABLE FORM:
MEDIUM IYPE: Floppy
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                                                                                                                                    NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                              NEW YORK
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ANTI-SENSE:
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; LCCAIION:
US-07-906-397A-5
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Pred. No. 4.1e-14;
0; Mismatches 24; Indels 0
                                                      PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/977,451
FILING DATE: 19-NOV-1992
PRIOR APPLICATION DATA:
APPLICATION DATA: 19-NOV-1992
FILING DATE: 26-JUN-1992
PRIOR APPLICATION DATA:
FILING DATE: 26-JUN-1992
PRIOR APPLICATION DATA:
FILING DATE: 26-JUN-1992
PRIOR APPLICATION DATA:
FILING DATE: 15-APR-1992
PRIOR APPLICATION DATA:
FILING DATE: 10-APR-1992
PRIOR APPLICATION DATA: US PCT/US92/02750
PRIOR APPLICATION DATA: US PCT/US92/02750
PRIOR APPLICATION DATA: US PCT/US92/02750
PRIOR APPLICATION DATA: US O7/813,593
FILING DATE: 12-BCC-1991
PRIOR APPLICATION DATA: US 07/793,065
FILING DATE: 15-NOV-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/728,913
FILING DATE: 28-JUN-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/679,666
FILING DATE: 02-APR-1991
ATTORNEY/AGENT INFORMATION:
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    APPLICATION NUMBER: US/08/252,517
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-645-1405
TELEFAX: 212-645-2054
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
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                31-0CT-1994
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Best Local Similarity 78.84
Matches 89; Conservative
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208..264
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265..4308
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EDNESS: double
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MOLECULE TYPE: CDNA
HYPOTHETICAL: NO
                                           CLASSIFICATION:
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; LOCATION:
US-08-252-517-5
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LOCATION:
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NAME/KEY:
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                                                                                                                                                                                                                               129 AGAGGGACGIGIGGICTIACGGAGTAITGCTGIGGGAAAICTICICCIIAGGT 181
                                                                         24.8%; Score 74.6; DB 1; Length 5406; 78.8%; Pred. No. 4.1e-14;
                                                                                                                   24; Indels
                                                                                                                   0; Mismatches
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mat_peptide
208..4308
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Best Local Similarity
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                                                                                                                   Matches
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3455 AGAGCGATGTGTGTTTTCGGTGTTGCTCTGGGAAATATTTCCTTAGGT 3507

129 AGAGCGACCTGTGGTCTTACGGAGTATTGCTGTGGGAAATCTTCTCCTTAGGT 181

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3395 CCCGACTCCCTITGAASIGGATGGCCCGGAAACCATTITGGACAGAGTATACACAATIC 3454
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                                                                                                                                                                                                                                                                                         Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                129 AGAGCGACGTGTGTTACGGAGTATTGCTGTGGGAAATCTTCTCCTTAGGF 181
                                                                                                                                                                                                                     24.8%; Score 74.6; DB 1; Length 5406; 78.8%; Pred. No. 4.1e-14; Live 0; Mismatches 24; Indels 0;
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US-09-021-324-5
Sequence 5, Application US/09021324
Sequence 5, Application US/09021324
Sequence 5, Application US/09021324
Sequence 5, Application US/09021324
Sequence 6, Sequence 7
TILLE OF INVENTION: TOTIPOTENT HEMATOPOIETIC SIEM CELL TITLE OF INVENTION: TOTIPOTENT US
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSED: Inclore Systems Incorporated SIREET: 180 Variox Street
CITY: New York
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APPLICATION NOWBER: US PCT/US52/02750
FILING DAIE: 02-APR-1992
FRIOR APPLICATION DAILA:
APPLICATION NOWBER: US 07/813,593
FRIOR APPLICATION DAIR: 24-EEC-1991
PRIOR APPLICATION DAIR: APPLICATION DAIR: APPLICATION NOWBER: US 07/793,065
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PRIOR APPLICATION DATE: TW 81102961
APPLICATION NUMBER: TW 81102961
FILING DATE: 15-APR-1003
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PRIOR APPLICATION DATA:
APPLICATION NUMBER:
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CLASSFEIGATION:
PRIOR APPLICATION DAIA:
APPLICATION NUMBER: US/07/977,451
APPLICATION NUMBER: 1952-11-19
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/906,397
FILING DATE: 26-UN-1992
PRIOR APPLICATION NUMBER: US PCT/US92/0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                         Conservative
                                                                                              sig_peptide
208..264
   mat_peptide
265..4308
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                                                                                                                                                                                                                               Query Match
Best Local Similarity
Matches 89; Conserv
NAME/KEY:
LOCATION:
FEATURE:
                                                                                                  NAME/KEY:
                                                                                                                                LOCATION:
                                                                                                                                                               US-08-601-891<sup>1</sup>5
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                                                                                                                                                                                             TITLE OF INVENTION: TOTIPOTENT HEMATOPOLETIC STEM CELL
TITLE OF INVENTION: RECEPTORS AND THEIR LIGANDS
NUMBER OF SEQUENCES: 10
CORRESPONDER ADDRESS:
ADDRESSEE: Inclone Systems Incorporated
STREET: 180 Variok Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE: Floppy disk
COMPUTER: IRM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DCS
SOFTAMER: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/601,891
FILING DATE: 15-FEB-1996
CLASSIFICATION: 330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US PCT/US92/02750
FILING DATE: 02-APR-1992
PRIOR APPLICATION DATA: APPLICATION NUMBER: US 07/813,593
FILING DATE: 24-DEC-1991
PRIOR APPLICATION DATA: US 07/793,065
FILING DATE: 15-NOV-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US 07/977,451
FILING DATE: 19-NOV-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/906,397
FILING DATE: 26-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US PCT/US92/05401
FILING DATE: 26-JUN-1992
FRIOR APPLICATION DATA:
APPLICATION NUMBER: US PCT/US92/05401
FILING DATE: 26-JUN-1992
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/K79 666
FILING NAME
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FILING DATE: 02-APR-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: TW 81102961
FILING DATE: 15-APR-1992
PRIOR APPLICATION DATA:
                                                                          ; Sequence 5, Application US/08601891; Patent No. 5747651
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Feit, Irving N. REGISTRATION NUMBER: 28,601
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-645-1405
                                                                                                                                          GENERAL INFORMATION:
APPLICANT: Lemischka, Ihor R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INFORMATION FOR SEQ ID NO: 5: SEQUENCE CHARACTERISTICS:
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TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ANTI-SENSE: NO FRAGMENT TYPE: N-terminal
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LOCATION: 208..4311
FEATURE:
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U.S.A.
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                    RESULT 10
US-08-601-891-5
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3355 CCGACICCCITIGAAGIGGATGGCCCCGGAAACCATTITGACAGAGTATACACAATTC 3454
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 5, Application PC/TUS9205401
GENERAL INFORMATION:
APPLICANT: Lemischka, Thor R.
TITLE OF INVENTION: TOTIPOTENT HEMATOPOIETIC STEM CELL
TITLE OF INVENTION: RECEPTORS AND THEIR LIGANDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY: U.S.A.

ZIP: 10014
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DCS
SOFTMARE: PATCATION Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/U5401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: IMCLONE SYSTEMS INCORPORATED
STREET: 130 VARICK STREET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LEM-3-PPPPPT
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ALIGNEY/AGENT INFORMATION:
NAME: Fell, ILVING N.
REGISTRATION NUMBER: 0.50,601
REFERENCE/COCKET NUMBER: 1.EM-:
IELECOMMUNICATION INFORMATION:
IELECOMMUNICATION:
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LENGTH: 5406 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: single
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208..4308
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208..4308
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STRANDEDNESS: single
                                                                                                                             CDS
208..4311
                                                               IOPOLOGY: linear MOLECULE TYPE: CDNA FEATURE:
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Matches 89; Conserve
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CLASSIFICATION:
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FEAIURE:
                                                                                                                             NAME/KEY:
LCCATION:
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FEATURE:
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; LOCATION:
PCT-US92-05401-5
                                                                                                                                                                                           NAME/KEY:
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                                                                                                                                                                                                                 LOCATION:
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                                                                                                                                                                         FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 24.8%; Score 74.6; DB 2; Length 5406; Best Local Similarity 78.8%; Pred. No. 4.1e-14; Matches 89; Conservative 0; Mismatches 24; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: LEMISCHKA, IHOR R.
TITLE OF INVENTION: Totipotent Hematopoietic Stem Cell
TITLE OF INVENTION: Receptors And Their Ligands
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: INCLONE SYSTEMS INCORPORATED
STREET: 180 VARICK STREET
CITY: NEW YORK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
SOFRATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/02750
CLASSIFICATION: 435
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                                         REFERENCE/DOCKET NUMBER: LEM-3-7P
TELECOMMUTCATION INFORMATION:
TELEBENOME: 212-645-405
TELEFAX: 212-645-2054
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ATTORNEY/AGENT INFORMATION:
NAME: FEIT, IRVING N.
REGISTRATION NUMBER: 28,601
      NAME: Felt, Irving N. REGISTRATION NUMBER: 28,601
                                                                                                     TELEFAX: 212-645-2054
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 5406 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                              ANTI-SENSE: NO
FRAGMENT TYPE: N-terminal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
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208..264
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265..4308
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                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: CDS
LOCATION: 208..4311
                                                                                                                                                                                                                                  TOPOLOGY: linear MOLECULE TYPE: cDNA HYPOTHETICAL: NO
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LOCATION:
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PCI-US92-02750-7
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69 CICGACIICCTCIGAAAIGGAIGGCTCCIGAATCTATCTIIGACAAAAICTACAGCACCA 128
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                                                                                                                                                                        APPLICANT: Ullrich, Axel
APPLICANT: Misau, Werner
APPLICANT: Misauer, Birgit
APPLICANT: Misauer, Birgit
APPLICANT: Gazit, Aviv
APPLICANT: Levitzki, Alex
IILE OF INVENTION: Fik-1 is A Receptor For Vascular
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE: Floppy disk CCMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DAIN:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Search completed: December 8, 2002, 07:52:31
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STREET: 1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        30,742
---- 7683-060
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APPLICATION NUMBER: US 08/193,829
FILING DATE: 09-FEB-1594
ATIGANEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/08/443,861
FILING DAIE: 22-MAY-1995
                                                                                                            ; Sequence 1, Application US/08443861
; Patent No. 5851999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: CORUZZÍ, LAURA A.
REGISTRAILON NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 76
IELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
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(212)869-9741
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: nucleic acid
STRANDEDNESS: unknown
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286..4386
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               unknown
                                                                                                                                                                                                                                                                                                                                                                                                            STAIE: New York COUNTRY: U.S.A. ZIP: 10036-2711.
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                                                                                                                                                           GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                             New York
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US-08-443-861-1
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                      Gabs
                                                                                                                                                           3455 AGAGCGATGTGTGGTCTTTCGGTGTGTTGTTGTTTTTCCTTAGGT 3507
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                    Indels
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TITLE OF INVENTION: TOTIPOTENT HEMATOPOIETIC STEM CELL TITLE OF INVENTION: RECEPTORS AND THEIR LIGANDS NUMBER OF SEQUENCES: 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE: Floppy disk
COMPUTER: 19m PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
FILING DATE: 19921116
  Pred, No. 4.le-14;
0; Mismatches 24;
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ADDRESSEE: Imclone Systems Incorporated
STREET: 180 Varick Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LEM-3-7PT
                                                                                                                                                                                                                                                                      Sequence 5, Application PC/TUS9209893 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY AGENT INFORMATION:
NAME: Feit, Irving N.
REGISTRATION NUMBER: 28,601
REFERENCE/DOCKET NUMBER: LEM-
TELECHMUNICATION:
TELEPHONE: 212-645-1405
TELEFAX: 212-645-2054
Best Local Similarity 78.8%;
Matches 89; Conservative (
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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TYPE: NUCLEIC ACID
STRANDEDNESS: double
TOPOLOGY: linear
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COMPUTER READABLE FORM:
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Best Local Similarity
Matches 89; Conserva
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FEATURE:
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PCT-US92-09893-5
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Gaps

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AAD15454 standard; DNA; 726 BP.
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Human KDR genomic
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Human polynucleoti
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/SIDS2/gcgdata/geneseq/geneseqn-emb1/NN1992.DAT:
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GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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                                                                                    OM nucleic - nucleic search, using sw model
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Human Flt4 recepto	AAA37816	21	1195	21.8	'n	.c.	
	AAC62210	21	1450		ď.	7	
yro	AAT03090	16		***	'n	<u>4</u> 4.	
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Human Flt4 recepto	37	21		ä	Ġ	.= **	
FLT4 receptor tyro	1206	17		ä	ď.	0.7	
a	AAC68952	22		\vdash	'n	isi Q	
Human Flt4/VEGFR-3		21			ď.	30 CF	
Human polynucleotí		24		· .	'n	3.7	
Human flk-2 cDNA.	AAX77515	50		CI	~	36	
£1k-2		18		CI.	7	ല	
e foeta		17) (r)) ~#	
1 £1k-2	9	91) (E)	
recepto	AAO81013	2 4		· ·		7 C	
Human flk-2 coding	AAQ35250	7	3501	22.3	67.2	⊕ ()	
flk-2	9	14		á	7.	9	
	~	16		\sim	7	28	
Ψ.	2	16		α	7.	27	
Protein tyrosine-k	-	16		\sim	7	25	
pTK gene LpTK25.	. ^	14		N	7.	25	
eceptor 1	AAV35039	19		O	7	24	
receptor	AAV39038	13		\sim	7.	23	
eceptor	AAV39042	5		O.		22	
Human receptor typ	_AAV39040	13		o.	~	2	
Human receptor typ		19		ď.	7	O	
Sequence of murine	AAQ64049	15				ς.	
Murine flk-1 recep	AAT72119	18		-		eo I E	
Mouse flk-1 cDNA.	AA075070	16			_	1.7	
Flk1 receptor prot	AAQ81014	16				10	
Murine flk-1 cDNA.	AA040916	14		_	-	10	
-	22	14			_		
$\vec{\cdot}$	AAQ53504	14		24.8		13	
flk-1 cDNA sequenc	AA029957	13		_:		. C	
Murine flk-1 cDNA.	AAX77516	20	5404				
Murine foetal live	AAT38735	17		24.8	_	10	

ALIGNMENTS

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Huma:: flt-1 gene, cytostatic; haemostatic; gene mapping; gynaecological; opth.lmological; rhoumatoid arthritis; endometriosis; angiogenic disease; diateric relinopathy; psoriasis; VEGFR-1; drug tierapy; pharmacogenetic; vasc.lar endothelial growth factor; single nucleotide polymorphism; SNP; cancer; medicament; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            /standard_name= "Single nucleotide polymorphism (SNP)"
                                                                                                                                                                                                                                                               Location/Qualifiers
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/star*
                                          Huma: flt-1 gene DNA fragment #3.
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The invention relates to novel sequence and polymorphisms in the human filt-1 gene. Filt-1 is one of the two receptors for vascular endothelial growth factor (VEGRel). The invention also relates to a method for diagnosing one or more single uncleotide polymorphism (SNP) in human filt-1 gene. The method is useful for assessing the predisposition and/or susceptibility of an individual to diseases mediated by an filt-1 ligand, to recognise individuals who are particularly at risk from developing these conditions, and in the development of new drug therapies that confirming are used in the diagnosis and treatment of the filt-1 gene. Filt-1 polymorphisms are used in the diagnosis and treatment of cancer and anglogenic diseases such as diabetic retinopathies, psoriasis, rheumatoid arthritis and endometriosis. Polymorphisms are also used in mapping the human genome and to elucidate the genetic component of the diseases, as genetic markers for this region in linkage studies. The nucleic acids are
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                                                                                                                                                                                                                                                                                                                                                                                                            Diagnosing single nucleotide polymorphism in human flt-1 gene, for assessing predisposition or susceptibility to diseases mediated by an flt-1 ligand, comprises determining the nucleic acid sequence at one or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            241 AATGTCCTTTGGTTGGACAGCCTTTAGATTAGAACCTACTGTAACAAAAAAACTCTTAAAG 300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 726 BP; 199 A; 165 C; 154 G; 207 T; 1 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 contains exon 24 and adjacent intron sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 8; Page 23; 30pp; English.
20-FEB-2001; 2001EP-0301489.
                                                                                       24-FEB-2000; 2000GB-0004232.
                                                                                                                                                                         (ASTR ) ASTRAZENECA AB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           more point positions
                                                                                                                                                                                                                                                                                                                                      WPI; 2001-608199/70.
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The invention relates to a method for inhibiting expression of a target gene (ABE)1566-ABE(31797) in a cell by introducing at least one oligoribonuclectide that has a double-stranded structure consisting of at most 49 sequential incleotide pairs, with at least part of one strand complementary with the target gene and has at least one end a single-stranded sequence of 1-4 n. The method provides oligoribonucleotides for antisense inhibition of gene expression useful e.g. for treating timours but the oligoribonucleotides may also be
                                                                                                                                             Human; HIV; HCV; gene expression; oligoribonucleotide; tumour; pathogen; Plasmodlum; virus; /iroid; eytokine; prion; antisense oligonucleotide; cytostatic; virucide; protozoacide; antibacterial; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3173 ATACTCGACTICCTCIGAAATGGATGGCTCCTGAATCIATGACAAAATCIACAGA 3232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          66 AGACTCGACTICCTUTGAAAIGGATGGCTCCTGAATCTATCIIIGACAAAAICTACAGCA 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Inhibiting gene expression in cells, useful for e.g. treating tumors, by introducing double-stranded complementary oligoRNA having unpaired
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   directed against genes present in pathogens (e.g. Plasmodium or viruses/viroids, pathogenic on humans, animals or plants) or against cytokine, id, developmental or prion genes. The method provides more effective inhibition of gene expression than use of known oligonucleotides, probably because the unpaired overhang increases stability and thus intracellular concentration.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  38.0%; Score 114.4; DB 24; Length 4017; 99.1%; Pred. No. 2.5e-26; Live 0; Mismatches 1; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 4017 BP; 1236 A; 915 C; 963 G; 963 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DNA encoding novel human diagnostic protein #6090.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Rost S, Hadwiger P;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 13; Page 68-69; 104pp; German.
                                                                                                             Human polynucleotide SEQ ID NO 95.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAS70286 standard; cDNA; 7680 BP.
ABL91752 standard; JNA; 4017 BP
                                                                                                                                                                                                                                                                                                                                             09-JAN-2001; 2001DE-1000586.
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Best Local Similarity 99.1
Matches 115; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Kreutzer R, Limmer S,
                                                                                                                                                                                                                                                                                                                                                                                                                        (RIBO-) RIBOPHARMA AG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2002-270454/32.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           terminal bases
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                                                                        28-MAY-2002
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                                      ABL91752;
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RESULT 2 ABL91752

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11-OCT-2001.

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The invention relates to a method for inhibiting expression of a target gene (ABL91658-ABL9197) in a cell by introducing at least one oligoribonucleotide that has a double-stranded structure consisting of at most 49 sequential nucleotide pairs, with at least part of one strand complementary with the target gene and has at least one end a single-stranded segment of 1-4 nt. The method provides
                                                          Human; HIV; HCV; gene expression; oligoribonucleotide; tumour; pathogen; Plasmodium; virus; viroid; cytokine; prion; antisense oligonucleotide; cytostatic; virucide; protozoacide; antibacterial; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         oligoribonucleotides for antisense inhibition of gene expression useful e.g. for treating tumours but the oligoribonucleotides may also be directed against genes present in pathogens (e.g. Plasmodium or viruses/viroids, pathogenic on humans, animals or plants) or against
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3194 CIGGCCICCCITIGAAAIGGAFGCCCCCAGAAACAATTTTGACAGAGIGIACACAATCC 3253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     69 CTCGACTTCCTCTGAATGGATGGCTCCTGAATCTATCTTTGACAAAAICTACAGCACCA 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Inhibiting gene expression in cells, useful for e.g. treating tumors, by introducing double-stranded complementary oligoRNA having unpaired
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cytokine, id, developmental or prion genes. The method provides more effective inhibition of gene expression than use of known oligonucleotides, probably because the unpaired overhang increases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Receptor tyrosine kinase; vascular endothelial cell growth factors; cancer; tumour; diagnosing; monitoring; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 129 AGAGCGACGTGTGGTCTTACGGAGTATTGCTGTGGGAAATCTTCTCCTTAGGT 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 4044 BP; 1163 A; 885 C; 1021 G; 975 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 76.2; DB 24;
Pred. No. 5e-14;
0; Mismatches 23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  stability and thus intracellular concentration.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hadwiger P;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A novel type III RIK gene - the KDR gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 13; Page 67-68; 104pp; German.
          Human polynucleotide SEQ ID NO 94.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAQ28272 standard; cDNA; 4071 BP.
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79.6%;
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Best Local Similarity 79.6
Matches 90; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Limmer ŝ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2002-270454/32.
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                                                                                                                                                                   Homo sapiens
                                                                                                                                                                                                                                                                  11-APR-2002.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Kreutzer R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAQ28272;
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AAQ28272
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ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention relates to isolated polynucleotide (1) and polypeptide (1) sequences. (1) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (11). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (1) is useful in gene therapy techniques (11). (11) is useful for genesting antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (11) and its binding partners are useful in medical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             diagnostics, foremsics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences. AAS64197-AAS94564 represent novel human diagnostic coding sequences of the invention.

Note: The sequence data for this parent did not appear in the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     126 CCAAGAGCGACGŢGTGGTCTTACGGAGTATTGCTGTGĠGAAATCTTCTCCTTAGGT 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
                  Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 7680;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New isolated polynucleotide and encoded polypeptides, useful in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ;
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Pred. No. 1.1e-25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 1; SEQ ID No 6090; 103pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                         Tang YT;
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98.3%;
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                                                                                                                                                                                                                                                                                            2000US-0540217.
2000US-0649167.
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                                                                                                                                                                                                                                                                                                                                                                                                                         Drmanac RT, Liu C,
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                                                                                                                                                                                                                                                                                                                                                                      (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                P-PSDB; ABG06099
                                                                                                                                              W0200175067-A2.
                                                                                                    Homo sapiens.
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RESULT 4 ABL91751 ID ABL9

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Length 4044;

W09214748-A. 03-SEP-1992

Key

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This nucleotide sequence encodes a novel receptor tyrosine kinase, termed KDR (see AAM80997), that is expressed on human endothelial cells. KDR is activated by vascular endothelial growth factor and caliates a mitogenic signal. It is implicated in clinical necangiogenesis. KDR cDNA was isolated from a human umbilical vein endothelial cell lambda phage CDNA library using a 576-pp DNA probe trait had been generated by PCR (see also AAV9980-53). The predicted protein product has amino acid differences from the previously published KDR sequence at positions 498 (Ala to Glu), 772 (Thr to Ala), 787 (dly to Arg), 835 (Asn to Lys), 848 (dlu to Val) and 1347 (Thr to Ser), producing a protein predicted by computer modeling to have higher activity and functionality. The invention also relates
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3134 CICGCCTCTTGAAAIGGAIGGCCCCAGAAACAATTTTTGACACAGIGIACACAAICC 3253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       65 CTCGACTICCTCTGAAATGGATGGCTCCTGAATCTATCTTTGACAAAATCTACAGCACCA 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             fragment encoding human KDR, a DNA fragment encoding the intracellular portion of KDR with or without a membrane anchor sequence, purified forms of associated human KDR, and human mutant forms of KDR. KDR, tusion proteins or fragments can be used in assays to identify antagonists and agonists of human KDR (claimed). Antagonists of KDR useful for treating diseases involving neonglogenesis e.g. diabetic retinal vascularization, cancers (e.g. brain, breast, etc.) and forms of inflammation e.g. rheumatoid artificials, psoriasis, contact dermatities and hypersensisitivity
                                                                                                                                                                                                                                                                                                                                                                                         Human receptor tyrosine kinase protein, KDR - useful e.g. to screen for antagonists useful to treat diseases involving necanglogenesis e.g. diabetic retinal vascularization, cancers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 antayonists/agonists and for gene therapy (e.g. by introducing a gene portion encoding a KDR protein containing functional ligand blading and membrane anchoring moieties but not tyrosine kinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3254 AGAGTGACGTCTGGTCTITIGGTGTTTGCTGTGGGAAATATITTCCTTAGGT 3306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                They are also useful to measure levels of human KDR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                129 AGAGCGACCIGIGGICITACGGAGIATIGCIGIGGAAAICIICICCIIAGGI 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The polynucleotides are useful to screen for KDR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 4071 BP; 1169 A; 894 C; 1027 G; 981 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 76.2; DB 20;
Pred. No. 5e-14;
0; Mismatches 23;
                                                                                                                                                                                                                                          Thomas KA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human polynucleotide SEQ ID NO 97.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ABL91754 standard; DNA; 4071 BP
                                                                                                                                                                                                                                          Tebben A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 1; Fig 1a; 69pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  25.3%;
79.6%;
                                                            98WO-US12569
                                                                                                                  97US-0050962
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        90; Conservative
                                                                                                                                                                                 MERI ) - MERCK & CO INC
                                                                                                                                                                                                                                          Mão X,
                                                                                                                                                                                                                                                                                                      1999-095333/08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                   P-PSDB; AAW80997
                                                            17-JUN-1598;
                                                                                                                     :8-JUN-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                28-MAY-2002
                                                                                                                                                                                                                                          Kendall RL,
23-DEC-1998.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   activity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              reactions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ABL91754;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ABL91754
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     G
                                                                                                                                                                                                                                                                                                                                                                                                                            ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This sequence represents a novel type III receptor tyrosine kinase gene. A labelled EcoRI-BamHI DNA segment derived from clone BTIII081.8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3194 CTGGCCTCCCTTTGAAATGGATGGCCCCAGAAACAATTTTTGACAGAGTGTACACAATCC 3253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             69 CYCGACTYCCTCTGAAATGGATGGCTCCTGAATCTATCTTTGACAAAATCTACAGCACCA 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Was used as a probe to rescreen a human endothelial cond library (HI10246) for 5'full length DNA segments of the gene from which the insert portion of BTIII081 B is derived. A synthetic probe designed from nucleotides 3297-3325 of BTII0818 Is then used to isolate more 3' full length clones. One of the clones, designated BTIII200.2 is cloned into pBUBLescript Ks and the synthetic oligonucleotide 105ACGCGCG ATG GA cloned, which contains the initial sequence Metility the first two amino acids encoded by the KDR gene, forming was sequenced, together with BTII1081.8, and BTIII129 to comprise the entire ORP of 4,068 nucleotides of the KDR gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    mitogen; necangiogenesis; angiogenesis; diabetic retinopathy;
breast cancer; brain cancer; inflammation; rheumatoid arthritis;
psoriasis; contact dermatitis; hypersensitivity; antagonist;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3254 AGAGTGACGTCTGTTTTCGTGTTTTGCTGTGGGAAATATTTCCTTAGGT 3306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 76.2; DB 13; Length 4071;
Pred. No. 5e-14;
); Mismatches 23; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  129 AGAGCGACGTGTGGTCTTACGGAGTATTGCTGTGGGAAATCTTCTCCTTAGGT 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DNA encoding type III receptor tyrosine kinase - useful for diagnosing the onset of cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              receptor tyrosine kinase; human; signal transduction;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 4071 BP; 1172 A; 894 C; 1024 G; 981 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human receptor tyrosine kinase KDR cDNA.
   Location/Qualifiers
1..4068
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAV99829 standard; cDNA; 4071 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 3; Fig 7; 101pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           25.3%;
                                                                                                                                                                                                                                                                                                                                                               (AMCY ) AMERICAN CYANAMID CO.
                                                                                                                                                                                                                                                                                                      91US-0657236.
                                                                                                                                                                                                                                       92WO-US01300.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match $ 25.3 Best Local Similarity 79.6 Matches 90; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                            Terman BI;
                                                            /*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 1992-316117/38.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   gene therapy; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              P-PSDB; AAR26999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  W09858053-A1
                                                                                                                                                                                                                                          20-FEB-1992;
                                                                                                                                                                                                                                                                                                      22-FEB-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     12-APR-1999
                                                                                                                                                                                                                                                                                                                                                                                                                            Carrion ME,
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Gaps

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AAV99829;

RESULT 6

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ò q AAV99829

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Length 4071;

11-APR-2002

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/*csg* b
/rote= "extracellular domain coding fragment (AAF83310)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention relates to determining whether a compound is capable of binding to a receptor protein complex comprising a vascular endothelial growth factor receptor? (VEGFR-2) receptor protein and a neuropilin-1 (NP-1) receptor protein. One method comprises introducing a sample comprising the compound to the receptor protein and allowing the compound to bind to the complex. Signaling through VEGFR-2 is enhanced in the presence of the NP-1 co-receptor. The methods of the invention can be used for identifying novel pro- and anti-anglogenic compounds. The present sequence represents the DNA encoding a human VEGFR-2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3263 CTCGCCTCCCTTTGAAATGGATGGCCCCAGAAACAATTTTTGACAGAGTGTACACAATCC 3322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      69 CICGACTICCICTGAAATGGATGGCTCCTGAATCTATCTTIGACAAAAICTACAGGCACCA 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Kinase insert domai: containing receptor; KDR; screening; inhibitor; vascular endothelia! growth factor; VEGF; angiogenesis; treatment;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /*tag= a /product= KDR /note= "kinase insert domain containing receptor"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Determining compounds which bind to a complex comprising vascular endothelial growth factor receptor-2 and Neuropilin-1 to provide superior pro- and anti-anglogenic agents
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3323 AGAGGACGICTGGTCITTTGGTGTTTTGCTGTGGAAATAITTTCCTTAGGT 3375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          129 AGAGCGACGTGTGTTACGGAGTATTGCTGTGGGAAATCTTCTCCTTAGGT 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 4225;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 4225 BP; 1204 A; 940 C; 1067 G; 1014 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 76.2; DB 22
Pred. No. 5.1e-14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                     Limberg BJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Example 1; Page 32-39; 82pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
/*tag= a
/product= "VEGFR-2"
71..2350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAV34763 standard; DNA; 4236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 25.3%;
79.6%;
                                                                                                                                                                                                                                                          26-0CT-2000; 2000MC-US29579.
                                                                                                                                                                                                                                                                                                                                                                                                                  Rosenbaum JS, Whitsker GB,
                                                                                                                                                                                                                                                                                                                                                               (PROC ) PROCIER & GAMBLE CO
                                                                                                                                                                                                                                                                                                           99US-0162367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity 79.6 Matches 90; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human KDR genomic DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2001-308686/32.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            P-PSDB; AAB62475
                                                                                                                                                     WC200131346-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens
                                                   misc_feature
                                                                                                                                                                                                                                                                                                              28-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             27-AUG-1958
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cancer; ss.
                                                                                                                                                                                                         03-MAY-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAV34763;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Key
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAV34763
                                                                                                                                                                                                                                                                                                                                                                                                                  ð
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ă
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention relates to a method for inhibiting expression of a target capene (ABL91658-ABL91797) in a cell by introducing at least one consisting of at coligoribonucleotide that has a double-stranded structure consisting of at most 49 sequential nucleotide pairs, with at least part of one strand complementary with the target gene and has at least one end a single-stranded segment of 1-4 nt. The method provides

CC complementary with the target gene and has at least one end a single-stranded segment of 1-4 nt. The method provides

CC digoribonucleotides for attisense inhibition of gene expression useful

CC of intercating tumours but the oligoribonucleotides may also be conference against genes present in pathogens (e.g. Plasmodium or viruses/viroids, pathogenic on humans, animals or plants) or against contoxine, Id, developmental or prion genes. The method provides more effective inhibition of gene expression than use of known coligonucleotides, probably because the unpaired overhang increases tability and thus intracellular concentration.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 at
     Human; HIV; HCV; gene expression; oligoribonucleotide; tumour; pathogen;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3194 CTGGCCTCCCTTTGAAATGGATGGCCCAGAAACAATTTTTGACAGAGTGTACACAATCC 3253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          69 CTCGACTICCTCTGAAATGGATGGCTCCTGAATCTATCTTTGACAAAATCTACAGCACCA 128
                        Plasmodium; virus; viroid; cytokine; prion; antisense oligonucleotide; cytostatic; virucide; protozoacide; antibacterial; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Inhibiting gene expression in cells, useful for e.g. treating tumors, by introducing double-stranded complementary oligoRNA having unpaired
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Receptor protein; vascular endothelial growth factor receptor-2; VEGFR-2; neuropilin-1; NP-1; co-receptor; human; angiogenic; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3254 AGAGTGACGTCTGGTCTTTTGGTGTTTTGCTGTGGGAAATATTTTCCTTAGGT 3306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 76.2; DB 24; Length 4071;
Pred. No. 5e-14;
0; Mismatches 23; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            129 AGAGCGACGTGTGCTCTTACGGAGTATTGCTGTGGGAAATCTTCTCCTTAGGT 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 4071 BP; 1169 A; 894 C; 1025 G; 983 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                     Hadwiger P;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers 70..4140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 13; Page 71-72; 104pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAF83308 standard; DNA; 4225 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                     Rost S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      25.3%;
                                                                                                                                                                                                                                                             09-JAN-2001; 2001DE-1000586.
                                                                                                                                                                                                                                                                                                              09-JAN-2001; 2001DE-1000586.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human VEGFR-2 encoding DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
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90; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                     Limmer S,
                                                                                                                                                                                                                                                                                                                                                                    (RIBO-) RIBOPHARMA AG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2002-270454/32.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           terminal bases
                                                                                                                                                        DE10100586-C1.
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                                                                                                            Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                     Kreutzer R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     09-JUL-2001
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AAF83308;

RESULT 8 AAF83308

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3355 CCCGACTCCCTITGAAGTGGATGGCCCCGGAAACCATTITGACAGAGIAIACACAATIC 3454
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      69 CICCACITICCICICAAAIGGAIGGCICCIGAAICTAICTITGACAAAAICIACAGCACCA 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present sequence encodes murine foetal liver kinase I (flk-1), a protein tyrosine kinase. Isolated antibodies, pref. monoclonal, raised against the extracellular portion of flk-1 can be used to assay for ilk receptors on the surface of haematopoletic stem cells, and to isolate positive cells. The antibodies can also be used as, or to obtain ligands, which stimulate the proliferation and/or differentiation of stem cells. The ligands can be used, e.g. for treating anaemia, or bone marrow damage resulting from cancer
                                                                                                                                                                                                                                                                                                                                                                   Anti-foetal liver kinase 2 (fik-2) antibodies - useful in assays, for isolating haematopoietic stem cells expressing receptor and for obtaining ligands
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Murine; flk-2; flk-1; cell isolation; fetal liver kinase; receptor; monoclonal; polyclonal; antibody; tyrosine kinase; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        24.8%; Score 74.6; DB 17; Length 5404; 78.8%; Pred. No. 1.8e-13; ive 0; Mismatches 24; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    129 AGAGCGACGTGTGGTCTTACGGAGTATTGCTGTGGGGAAATCTTCTCCTTAGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 5404 BP; 1411 A; 1297 C; 1423 G; 1273 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure; Columns 51-62; 50pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
208..4311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /*tag- a /product= "flk-1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAX77516 standard; cDNA; 5404 BP.
                                                       910S-0679666.
910S-0728913.
910S-0793065.
910S-0813593.
920S-0906397.
                                                                                                                                                          920S-0975049.
93US-0055269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    chemotherapy, or radiation.
9105-0579666
                                                                                                                                                                                                 94US-0252517
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       05-AUG-1999 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     89; Conservative
                                                                                                                                                                                                                                        NCIECNIE PRINCEION
                                                                                                                                                                                                                                                                                                               WPI; 1996-392678/39.
P-PSDB; AAT38735.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sest Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Murine flk-1 cDNA
                                                                                                                                                                                                                                                                            Lemischka IR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US5912133-A.
    02-APR-1991;
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                                         19-NOV-1992
                                                                                                                                                            .2-NOV-1992
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                                                                                                                                                                                10-APR-1993
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                            This sequence encodes a novel human growth factor receptor, kinase insert domain containing receptor or KDR. This receptor is capable of binding to the vascular endothelial cell growth factor, VEGF and is used in a screening assay which identifies compounds that inhibit VEGF action on KDR. Such compounds which inhibit binding of VEGF to the KDR may inhibit anglogenesis and thus be useful for treating caneer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1194 CICGCCICCTITGAARGGATGGCCCCAGAAACAATTTTTGACAGAGTGTACACAATCC 3253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      69 CICCACITCCICTGAAAIGGAIGGCICCIGAAICTAICTITGACAAAATCIACAGCACCA 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                    Screening assay for vascular endothelial cell growth factor antagonists - using recombinant cells expressing receptor protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       · .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Murine; foetal liver kinase 1; flk-1; protein tyrosine kinase; monoclonal; antibody; extracellular domain; receptor assay; habamatopoletic stem cell; ligand; stimulation; proliferation; differentiation; treatment; anaemia; bone marrow damage; cancer chemotherapy; radiation; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    129 AGAGCGACGTGTGGTCTTACGGAGTATTGCTGTGGGAAATCTTCTCCTTAGGT 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        25.3%; Score 76.2; DB 19; Length 4236; 79.6%; Pred. No. 5.1e-14; Ive 0; Mismatches 23; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 4236 BP; 1216 A; 938 C; 1062 G; 1020 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Murine foetal liver kinase 1 cDNA.
                                                                                                                                                                                                                                                                                                                                                                                 Claim 1; Fig 7A-M; 51pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAT38735 standard; cDNA; 5404 BP
                                                                                                                                                                                    (AMCY ) AMERICAN CYANAMID CO.
                                                                                                                                               97US-0810116.
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265..4308
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208..264
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90; Conservative
                                                                                                                                                                                                                           Carrion ME, Terman BI;
                                                                                                                                                                                                                                                                WPI; 1998-361682/31.
                                                                                                                                                                                                                                                                                     P-PSDB; AAW59275
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                                                                                        25-FEB-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                              2550 CATICICGIACGGACCGITAAGCGGGCCAAIGAAGGGGAACIGAAGAGACAGGCTACITGIC 2609
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2610 ALIGICALGGALCCAGALGAALIGCCCTTGGALGACGCTGGAAGGCTTGCCTAIGA 2669
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2910 GGCCIGCACCAAGCCGGGAGGCCTCICAIGGIAIIGH HHI HI HI HIHHH 2969
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1098 TCTCTCCAACTACCTCAAGAGCAAACGIGACTTATTTTTTCTCAACAAGGATGCAGCACT 1157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2970 cctarcaacitactracegeccaagagaaaregarriigricccraraagaggaaggegc 3029
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ACACATGGAGCCTAAGAAAGAAAAATGGAGCCAGGCCTGGAACAAGGCAAGAAACCAAG 1217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1218 ACTAGATAGCGTCACCAGCAGCGAAAGCTTTGCGAGCTCCGGCTTTCAGGAAGATAAAAG 1277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1278 ICIGAGIGAIGIIGAGGAAGAGGAGGAIICIGACGGIIICIACAAGGAGCCCAICACIAI 1337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GGAAGAICIGAITICITACAGITITCAAGIGGCCAGAGGCAIGGAGITCCIGICTICCAG 1397
                                                                                                                                                                                                                                                                                           2430 IGGCTGIGCAAGAGGGGAGAGGCTGTTCATAATAGAAGGTGCCCAGGAAAAGAAGACTI 2489
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1038 AGCCIGCACCAAGCAAGGAGGCCCICIGAIGGIGAITGIIGAAIACIGCAAAIAIGGAAA 1097
                                                                                    2310 caacgagaccciggragaagarrcaggcarrgragagaaggaarcggaaccrgac 2369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TECCAGCAASIGGGAGTITGCCCGGGAGAGITAAACTGGGCAAATCACTTGGAAGAGG 857
                                                                                                                                                                                                                                                                                                                                             521 GGAGCIGAICACICIAACAIGCACCIGTGIGGCIGCGACICTCTICIGGCICCIAIIAAC 680
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            681 CCTCCTTATCCGAAAAAGAAAAGGTC---TTCTTCTGAAATAAAGACTGACTACCTATC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   738 AAITATAAIGGACCCAGAIGAAGTICCTIIGGATGAGGAGIGIGAGGGGCTCCCIIAIGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      858 GGCTTTTGGAAAAGTGGTTCAAGCATCAGCATTTGGCATTAAGAAATCACCTACGTGCCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        918 GACTGTGGCTGTGAAAATGCTGAAAGAGGGGGCCACGGCCAGCGAGTACAAAGCTCTGAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2730 AACAGTAGCCGTCAAGATGTTGAAAGAAGAGGAGCAACACACAGGAGCATCGAGCCTCAT
                                                                                                                                                                                                                                                                                                                                                                              2490 GGAAGICATIAICCICGICGCACIGCAGIGALIGCCAIGIICTICIGGCICCTICITGI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GACTGAGCTAAAAATCTTGACCCACATTGGCCACCATCTGAACGTGGTTAACCTGCTGGG
                              2190 GCGCATGGCACCCATGATCACCGGAAATCTGGAGAATCAGACAACAACAACATTGGCGAGAC
                                                                                                                                                                                                                          TCAGGAAGCACCATACCTCCTGCGAAACCTCAGTGATCACACAGTGGCCATCAGCAGTTC
                                                                CACCACIIIAGACIGICAIGCIAAIGGIGICCCCGAGCCICAGAICACIIGGIIIAAAAA
                                                                                                                                     441 CAACCACAAAATACAACAAGAGCCTGGAATTATTTTAGGACCAGGAAGCAGCACGCTGTT
                                                                                                                                                                                                         501 TATTGAAAGAGTCACAGAAGAGGATGAGGTGTCTATCACTGCAAAGGCCACCAAGCAAA
                                                                                                                                                                                                                                                                         551 GGGCTCTGTGGAAAGITCAGCATACCTCACTGTTCAAGGAACCTCGGACAAGTCTAATCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2070 carcifgarigiogcarificagaargccrcrcrdcaggaccaaggcgacraigiffgcrc 2129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2130 IGCICAAGAIAASAAGACCAAGAAAAGACATIGCCIGGICAAACAGGICAICAICCIAGA 2189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                261 AGCCAGGAAIGTAIACACAGGGGAAGAAICCICCAGAAGAAAGAAAITACAAICAGAGA 320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             201 CACTCTTAATCTTACCATCATGAATGTTTCCCTGCAAGATTCAGGCACCTATGCCTGCAG 260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Murine flk-2 receptor protein tyrosine kinase - used to stimulate proliferation and/or stimulation of primitive mammalian haematopoietic stem cells in vitro or in vivo.
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                                                                                                                                                                                                               retal liver kinase-1; flk-1; protein tyrosine-kinase receptor; hematopoiesis; stem cell; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 5406 BP; 1412 A; 1298 C; 1423 G; 1273 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
     3687 CCTCCTGCAAGCAAATGCGCAGCAGGATGGCAAAGACTATAT 3728
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         33.7%; Score 708.4; DB 16;
65.0%; Pred. No. 1.3e-204;
tive 0; Mismatches 576;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure, Fig. 3A-31; 69pp; English.
                                                                                                                                                                                                                                                                                                                Location/Qualifiers
208..4311
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208..254
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92US-0906397.
92US-0975049.
92US-0977451.
93US-0055269.
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265..4308
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                                                                                                                                                            (first entry)
                                                                                        AAQ79070 standard; cDNA;
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26-JUN-1992;
12-NOV-1992;
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                                                                                                                                                                                           Mouse flk-1
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15-NOV-1991;
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AA079070
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PAT 17-0CT-2001 linear Har 3/15/99 DNA AR157385 1745 bp Sequence 1 from patent US 6245512. AR157385 AR157385.1 GI:16218320

Unknown.

SOURCE

REFERENCE AUTHORS TITLE JOURNAL FEATURES

ACCESSION VERSION KEYWORDS

RESULT 1
AR157385
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DEFINITION

(bases 1 to 1745)
Williams L.T. and Morishita,K.
Promoter for VEGF receptor.
Patent: US 6745512-A 1 12-JUN-2001;
Location/Qualifiers Unkhown. Unclassified.

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Location/Qualifiers
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1 (bases 1 to 1745)
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A novel promoter for vascular endothelial growth factor re
(flt-1) that confers endothelial specific gene expression
J. Biol. Chem. 270 (46), 27948-27933 (1995)
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                                                        http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 13, constructed by the Sanger Centre Chromosome 13
Wp:, WORMPEP; Information on the WORMPEP
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hote-"LJMC4 repeat: matches 7645. .7820 of consensus"
                                                                                                                                                                                                                                                                                                                                         IMPORTANT: This sequence is not the entire insert of clone RP11-9566 It may be shorter because we sequence overlapping sections only once, except for a 100 base overlap. The true right end of clone RP11-9566 is at 102119 in this sequence. The true left end of clone RP11-57274 is at 59065 sequence. The true right end of clone RP11-57274 is at 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1685. 8771
note="MER5B repeat: matches 84. 178 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            of consensus'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .2742 of consensus'
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8655. 8771
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       note="AluSx repeat: matches 1. .300 of consensus"
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Anotes"AluSp repeat: matches 1. .305 of consensus' 3751 .18781 .18781 .18781 .18781 .18781 .18781 .18781 .18781 .18781 .18781 .18781 .18781 .18781 .18781 .18781 .18781 .18781 .18781 .18781 .18781 .18781 .18781 .18781 .18781 .18781 .18781 .18781 .18781 .18781 .18781 .18781 .18781 .18781 .18781 .18781 .18781 .18781 .18781 .18781 .18781 .18781 .18781 .18781 .18781 .18781 .18781 .18781 .18781 .18781 .18781 .18781 .18781 .18781 .18781 .18781 .18781 .18781 .18781 .18781 .18781 .18781 .18781 .18781 .18781 .18781 .18781 .18781 .18781 .18781 .18781 .18781 .18781 .18781 .18781 .18781 .18781 .18781 .18781 .18781 .18781 .18781 .18781 .18781 .18781 .18781 .18781 .18781 .18781 .18781 .18781 .18781 .18781 .18781 .18781 .18781 .18781 .18781 .18781 .18781 .18781 .18781 .18781 .18781 .18781 .18781 .18781 .18781 .18781 .18781 .18781 .18781 .18781 .18781 .18781 .18781 .18781 .18781 .18781 .18781 .18781 .18781 .18781 .18781 .18781 .18781 .18781 .18781 .18781 .18781 .18781 .18781 .18781 .18781 .18781 .18781 .18781 .18781 .18781 .18781 .18781 .18781 .18781 .18781 .18781 .18781 .18781 .18781 .18781 .18781 .18781 .18781 .18781 .18781 .18781 .18781 .18781 .18781 .18781 .18781 .18781 .18781 .18781 .18781 .18781 .18781 .18781 .18781 .18781 .18781 .18781 .18781 .18781 .18781 .18781 .18781 .18781 .18781 .18781 .18781 .18781 .18781 .18781 .18781 .18781 .18781 .18781 .18781 .18781 .18781 .18781 .18781 .18781 .18781 .18781 .18781 .18781 .18781 .18781 .18781 .18781 .18781 .18781 .18781 .18781 .18781 .18781 .18781 .18781 .18781 .18781 .18781 .18781 .18781 .18781 .18781 .18781 .18781 .18781 .18781 .18781 .18781 .18781 .18781 .18781 .18781 .18781 .18781 .18781 .18781 .18781 .18781 .18781 .18781 .18781 .18781 .18781 .18781 .18781 .18781 .18781 .18781 .18781 .18781 .18781 .18781 .18781 .18781 .18781 .18781 .18781 .18781 .18781 .18781 .18781 .18781 .18781 .18781 .18781 .18781 .18781 .18781 .18781 .18781 .18781 .18781 .18781 .18781 .18781 .18781 .18781 .18781 .18781 .18781 .18781 .18781 .1
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8151. .3398
//octe="MIR repeat: matches 2. .252 of consensus"
                                                                                                                 mapping Group. Further information can be found at http://www.sanger.ac.uk/MBP/Chri3 RP11-9565 is from the library RPC1-11.1 constructed in Pieter de Jong. For further details see http://www.chori.org/bacpac/home.htm
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    copies 4 mer gtgt 100% conserved
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6387
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/note-112 copies 3 mer tta 94% conserved"
9958. 10079
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15580. .15698
/note="7 copies 17 mer 74% conserved"
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15701
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351. .979
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1. .102119
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/clone="RP11-95G6"
   SWISSPROT; Tr:, TREMBL; Watabase can be found at
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

This sequence was finished as follows unless otherwise noted: all
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRI 09-MAY-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        On May 11, 2001 this sequence version replaced gi:13274246.

During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission
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Human DNA sequence from clone RP11-95G6 on chromosome 13, complete
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    in the feature table with their source databases: Em:, EMBL; 5x:,
                                                                                                                                                                                                                                                   1039
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Submitted (19-MAY-2001) Sanger Centre, Hinxton, Cambridgeshire,
CBIO 15A, UK. E-mail enquiries: humquery@sanger.ac.uk Clone
requests: clonerequest@sanger.ac.uk
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   860 GGGTGGAGGAGTCTGCAAGGAITTCCIGAGCGCGAIGGGCAGGAGGAGGGCAAAGGGCA 919
                                                                                                                                                                                                                                                   980 AGCACCICCCACGCGCGCCCCGGGCCACCCGGCCCICGICGGCCCCCGCCCCCTCI
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                                                           421 AGAGGGGGGGGGGAGCAAAGACCTGAACTGCCGGGGCGGGGCTCCCGGGCCCGCGCGTCGC
                                                                                                                                                                                          AGCACCICCCCACGCGCGCTCGGCCCCGGGCCACCGGCCCTCGTCGGCCCCCGGCCCTCT
                                                                                                                                                                                                                                                                                                                  541 CCGIAGCCGCAGGGAAGCGAGCCIGGGAAGAAGAAGAGGGIAGGIGGGGAGGCGGAIGAG
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                                                                                                601 GGGIGGGGGACCCCIIGACGICACCAGAAGAGGIGCCGGGGIAGGAAGIGGGCIGGGGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GI:14018246
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AL139005/c
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KEYWORDS
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/note="L1MB8 repeat: matches 2311. .2594 of consensus" 47454. ,47743 /note="L1MBB repeat: matches 2594. .3347 of consensus" 48489. .48761 7.01e="MIR repeat: matches 1. .94 of consensus"
17832. 17897
17845. 18023
17845. 18023
17046-L2 repeat: matches 2567. .2739 of consensus"
18059. 18137
18144. 18777
18344. 18777
19344. 19378 note="AluSg/x repeat: matches 202. .305 of consensus" note-"Alura8 repeat: matches 134, .210 of consensus' 21868. .22166 note="FLAM_A repeat: matches 51. .128 of consensus" 1009. .21072 Voca- Will repeat: matches 14. .241 of consensus. 10593. .40743 Anote- Will repeat: matches 2647. .2699 of consensus. Thote- Will repeat: matches 3. .420 of consensus. 16596. .43167 Anote- Will repeat: matches 77. .140 of consensus. 14367. .44442 consensus /note="AluSx repeat: matches 1. .292 of consensus" 47744. .48488 /note="Alusx repeat: matches 1. .275 of consensus" 48762. .50491 .2701 of consensus' .2710 of consensus /note="MER50 repeat: matches 1. .709 of consensus" 44954. .45088 .308 of consensus" .302 of consensus? Total Tepeat: matches 1. .299 of consensus. 75148. .2236
Thotal Mik repeat: matches 52. .147 of consensus. 72732. .27532. .27532. .313 of consensus' .299 of consensus? .262 of consensus? .141 of consensus? mote="MIR repeat: matches 85. .258 of consensus" (0842. .2092) note="MIR repeat: matches 2. .241 of consensus" [9810. .1997] .5525. 15704 Gote="20 copies 4 mer tott 87% conserved" 5708. 16014. .129 of /note="22 copies 2 mer ac 90% conserved" 45996. .46035 note="34 copies 2 mer tt 66% conserved" 9702, 30027 note="MIR repeat: matches 54. .140 of 0565. .21034 .208 of /note="FLAM_C repeat: matches 2. 15992. .46035 19702, .30027 Chotem 12 repeat: matches 2356. 1857. .31999 Joost. .96016 /note="MER3 repeat: matches 1. . .37895. .38193 /note="Aluxs repeat: matches 1. (0664. .40284 note="AluSq repeat: matches 1. /note="AluJb repeat: matches 1.
22892, .23190 note="L2 repeat: matches 2648. 19350. ,19582 1857. .31555 note="MIR repeat: matches 25. 5831. .36016 repeat: matches 1. /note="MIR repeat: matches 14. 44173, ,44831 /note="10 copies 4 mer 17173. .47453 /note="AluSx I 15022. .16126 29442 15126 repeat_region

99118 GCGGAAAAAGACACGGACACGCTCCCCTGGGACCTGAGCTGGTTCGCAGTCTTCCCAAAG 99059 99058 GTGCCAAGCGTCAGTTCCCCTCAGGCGTTCAGGGCGTTGTGCTTGTGCCTTGTGCCAGGGT 98999 98699 98639 98579 98398 CICCGGIGCCIICCIAGACIICICGGGACAGICIGAAGGGGICAGGAGCGGCGGGACAGC 98939 540 ANGSTIATAAATGGCCCCGCGCTCGGCTGCTTCATCGAGGTCGCGGGGGGGCTGGGA 720 420 consensus, GIECCAAGCAAGCGICAGTICCCCICAGGCGCTCCAGGTICAGIGCCTIGIGCCGAGGGT 120 GCGGGRAGGAGGCAGGCAAGGGGAGACAGCCGGACTGCGCCTCAGTCCTCCGTGCCAAGAAC 240 ACCGICGCGGAGGCGCGGCCAGCIICCCIIGGAICGGACIIICCGCCCTAGGGCCAGGC 300 Gaps 1 GCCGAAAAAGACACGGACACGCTCCCCTGGGACCTGAGCTGGTTCGCAGTCTTCCCAAAG 60 /note="Alujb repeat: matches 1. .285 of consensus" 50781. [51024 98758 GGGTGGAGGAGTCTGCAAGGATTTCCTGAGGCGGGATGGGCAGGGGGCAAGGGCA PB578 CCGIAGCCGCAGGGAAGCGAGCCTGGGAGGAAGAAGAAGGGGTAGGTGGGGGAGGAGGGATGAG /note="Alusx repeat: matches 1. .308 of consensus" 54900. 54988 /note="42 copies 2 mer gg 64% conserved" 55026. 55061. CCGIAGCCGCAGGGAAGCGAGCCTGGGAAGAGAAGAGGGGTAGGTGGGGAGGCGGATGAG /note="Alujo repeat: matches 1. .295 of consensus" 53786. .53900 AGAGGGGGGGAGCAAAGACCCTGAACCTGCGGGGCCGCGCTCCCGGGGCCGGGGCCGCGTCGCC GGGTGGGGGACCCCTTGACGTCACCAGAAGGAGGTGCCGGGGTAGGAAGTGGGCTGGGGA GEGIGGAGGGAGICIGCAAGGAIIICCIGAGCGCGATGGGCAGGAGGGGGCCAAGGGCA GGCGGAGCTTCAGCCTTGTCCCTTCCCCAGTTTCGGGCGGCCCCCCAGAGCTGAGTAAGCC Length 102119; 50781. 51024 /note="1.1MBB repeat: matches 5028. 5274 of 51044. 51179 /note="8 copies 17 mer 66% conserved" 51190. 52061 21190. .32001 700t=7.11MB repeat: matches 5271. .6171 of 52293. .5277 repeat: matches 3347. :5028 of 2 copies 4 mer agga 68% conserved" 54138 Indels /note="5 copies 23 mer 68% conserved" 53788. .53875 /note="22 copies / mr-DB 9; Score 939.4; DB 9; Pred. No. 7.8e-144; 0; Mismatches. 1; 54044. 54138 /note="MIR repeat: matches 46. 54435. 54742 99.88; Conservative Similarity repeat_region repeat_region repeat_region repeat_region repeat_region repeat_region repeat_region repeat_region repeat_region repeat_region repeat_region Matches 940; Query Match Best Local S 98818 98638 501 661 15 241 98818 421 86986 481 541 301 361 121 181 00 g a d 쉱 8 DC g CD 9 ã 8 õ ő 8 ô 6 8 6

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508 GENERALTINGCONTRESTORGCOCCOCCONTRACCOCCAGGGAAGC-GAGCOTGG
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AX251105
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Promoter of human flt gene encoding receptor type tyrosine kinase.
E10168
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CI2N15/09, A61K31/70, A61K48/00, CI2N5/10, C12P21/02//C07821/04.
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                                          9839B GCGCGCAGGCGGACACTCCTCGGCTCCTCCCGGCAGCGCGCGGCTCGGACGGG
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                                                                                                                                                                                           /organism='Homo sapiens'
/tissue_type='placenta'
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Patent: JP 1995289263-A 1 07-NOV-1995;
DAI ICHI SETTARU CO LID
ASS HOMO SEPIENS (human)
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/db_xref="taxon:9606"
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  DNA (Homo sapiens)
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                                                                                                                          4272 GICGAAAAAGAIACGGAIACGIIIIIIGGGAIIIGAGIIGGIICGIAGIIIIIIAAAG
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Pred. No. 1.76-90:
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/note="chemically treated genomic
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4932 AAGGIIAIAAAICGIIIICGIIIICGGIIGIIIIIIAICGAGGIICGCGGGAGGIICGGA 4993
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/db_xref="taxon:3250"
/note="chemically treated genomic DNA (Homo sapiens)"
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Diagnosis of diseases associated with signal transduction
Patent: WO 0200526-A 103 03-JAN-2002,
Epigenomics AG (DE)
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Diagnosis of diseases associated with cell signalling
Patent: WO 0202807-A 105 10-JAN-2002;
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CICCGGIGCCIICCIAGACIICICGGGACAGICIGAAGGGGICAGGAGGGGGGGACAGC
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Diagnosis of diseases associated with anglogenesis
Patent: WO 0246454-A 93 13-JUN-2002;
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                                 0; Mismatches 205;
Score 613; DB 6;
Pred, No. 1.7e-90;
 65.18;
78.28;
                                      Conservative
                    Similarity
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SOURCE

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NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bom.tmc.edu/docs/Genbark_draft_data.html) (see http://www.hgsc.bom.tmc.edu/docs/Genbark_draft_data.html) consists 6.57 contribs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Saps Letween the contigs are represented as runs of N but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                    Sequencing vector: Plasmid; Chemistry: Dye-terminator Big Dye: 160% of reads Assembly program: Phrapy version 0.590% of consens, aquality: 101711 bases at least 0.30 consens.s quality: 106747 bases at least 0.30 consens.s quality: 110016 bases at least 0.20
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                                                                                                    Rattus norvegicus clone CH230-448N2, *** SEQUENCING IN PRUGRESS ACTORAGE.
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                                                                                                                                                                                                                                                                                                            Eukaryota, Métazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murimse,
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Web site: http://www.hgsc.bcm.tmc.edu/
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Center clone name: CH230-448N2
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Worley, K.C.
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Db 30630 TCTTGTCCTATGCAGA 30614
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Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Bukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Marmalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 4017)

Herley,M.T., Yu,Y., Whitney,R.G. and Sato,J.D.

Characterization of the VEGF binding site on the Fit-1 receptor

Blochem. Biophys. Res. Commun. 262 (3), 731-738 (1999)

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Yu,Y., Whitney,R.G. and Sato,J.D.
Direct Submission
Submitted (CoMAY-1999) Adirondack Biomedical Research Institute, 10 Old Barn Rd., Lake Placid, NY 12946, USA
Location/Qualifiers
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Pred. No. 3.5e-23;
0; Mismatches 1; Indels 0;
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Ribopharma AG (DE)
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/db_xref-"taxon:9606
/cell_type="endothelium"
/tissue_type="umbilical vein"
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                                                                                                  RESULT 4
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Pred. No. 4.3e-26;
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gap of unknown l
contig of 5044 b
gap of unknown l
contig of 3468 b
gap of unknown l
                        unknown
of 2482 h
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of 1760 b
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of 1883 b
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of 2078 b
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unknown ]
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gap of unknown
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gap of unknown
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gap of unknown
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gap of unknown
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Matches 158; Conservative
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3 (bases 1 to 7680)
Han, H.J., Fujiwara, T., Shin, S. and Nakamura, Y.
Dinucleotide repeat polymorphism in the 3' non-coding region of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /LTGAB 1 at 10.0. MVSYMDTGVILCALLSCILLIGSSSGSKIKDPELSIKGTGHING
AGGTLHIOCRGEAAHKWSLPEWYSKEESRISTIKSCGRNKQFCSTLTINTAQANHT
GFYSCKYLAVPTSKKETEBAIVIFISDIGAPFVEMYSEPIPIHHWTGSRELVIPERV
TSPHIYTHIKREPLDTLIPEGKRIHUMSSKGFIISNATYÆFIGLICREATVAGHIXKT
NYLTHRQTNTIIDVQISTPRPVKLLRGHTLVINGTAITPHRQTNTIIDVQISTPRPWKLLRGHTVINGTAITPHRQTNTIIDVQISTPRPWKLLRGHTLVINGTAITPHRTGNATWSYPDEKNKRA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MAIIEGKNKMASTLVVADSRISGIYICIASNYGTVÖRNISFYITDVPNOFHYNLEKN
PTEGEDLKLSCTVNKFLYRDVFWILLRTVNNRTMHYSISKQKMAITKEHSITLNLTIH
NYSLODSGIYACRARNYTGEEILLGKKEITIRDQEAFYLLINLSCHTAATSSSFILDC
HANGYPEPQITWRKNNHKIQQEPGITLGPGSSTIFIERVTEEDEGGYHGKARJNKGSY
ESSAYLTVQGISEKSNLELITLCTCVAATLFWILLILLIKKMKRSSSEIKTDYLSII
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SVRRIDOSNSHANIFYSVLTIDKAQNKDKGLYICRVRSGBSFKGVNTSVHIYDKAFI
IVKHRKQQVLETVAGKRSYRLSMKVKAFPSPEVVWLKLGLPAIEKSARYLTRGYSLII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KDVTEEDAGNYTILLSIKOSNVFKNLTATLIVNVKFOIYEKAVSSFPDPALFIGSRO
ILTCTAYGIPQPTIKWFWHPCNHNHSEARCDFCSNNEESFILDADSNMGNRIESITQR
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GNLSNYLKSKRDILFFLNKDAALHMEPKKEKMEPGLEGGKKPRLDSVTSSESFASSGFQ
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FAELVEKLGDLLQANVQQDGKDYIPINAILIGNSGFIYSTPAFSEDFFKESISAPKFN
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SKFKASLKIDLRVISKSKESGLSDVSRPSFCHSSCGHVSEGKRRFTYDHAELERKIAC
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                                                                                                                                                                                                        Data kindly reviewed (20-JUL-1990) by Shibuya M.
Location/Qualifiers
1. .7680
                                                                                                                                                                                                                                                                                                                                                                                                                              250. .4266
/note-"flt gene product (AA 1-1338)"
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                                                                                                                              Genet. 2 (12), 2204 (1993)
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/protein_id="CAA35946.1"
/db_xref="G1:31432"
                                                                                                                                                                                                                                                                                /organism-"Homo sapiens"
/db_xref-"taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                       /tissue_type="placenta"
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/map="13q12"
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TVKHRKQQVLETVAGKRSYRLSMKVKAFPSPEVVWIKDGLPATEKSARVLIRGYSLII
KDVTEEDAGNYTILLSIKQSNVFKNLTATLIVNVKPQIYEKAVSSFPDPALYFLGSRQ
                                                                                                                                                                                                                                                                                                                                                                                                                 ILTCTAYGIPQPTIKWFWHPCNHNHSEARCDFCSNNEESFILDADSNMORFIESITOR
MAIIEGKNKMASTLVVADSRISGIYICIASNKVGTVGRNISFYITDVPWGFHVNLEKM
PTEGEDLKLSCTVNKFLYRDVTWILLRTVNNRTMHYSISKQKMAIIKEHSIILNLTIM
                                                                                                                                                                                                                   /trānslation="musywdtgvilcallscinilosssgsklkdppelsikolohimg
Aggylhlqcrgeaahkwslpemyskespelsirksacgrngkgfcstltniagakht
GFYSCKYLAVPTSKKKETESAIYIFISDIGRPFVEMYSEIPEIIHMIEGRELVIPCRV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NVSLQDSGTYACRARNVYTGEETLQXKETT1KDQEAPYLLTNLSDHTVATSSSTTLDC
HANGVPEPQITWEKNNHKIQQEPGITLGPGSSTLFTERVTEEDEGVYHCKATWQKGSV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ESSAYLTVQGTSDKSNLELITLTCTCVAATLFWLL.TLF1RKWRRSSSE1KTDYLS11
MDPDEVPLDEQCERLPYDASKWEFARERLKLGKSLGRGAFGKVVQASAFG1KKSF1CR
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SKPKASLKIDLRVTSKSKESGLSDVSRPSFC#SSCGHVSEGKRRFTYDHAELERKIAC
                                                                                                                                                                                                                                                                                                ISPNITVTLKKFPLDTLIPDGKRIIMDSRKGFIISNATYKEIGLLTCEATVNGHLYKT
                                                                                                                                                                                                                                                                                                                    NYLTHROTNTIIDVOISTPRPVKLLRGHTLVLNCIATTPLNTRVQMTWSYPSEKNKRA
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GNLSNYLKSKRDLFFLNKDAALHMEPKKEKMEPGLEQGKKPRLDSVISSESFASSGFQ
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SENNVVKIODFGLARDIYKNPDYVRKGDIRLPLKMMAPESIFDKIYSIKSOVMSYGVL
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Nucleotide sequence and expression of a novel human receptor-type tyrosine kinase gene (fit) closely related to the fms family 90221591
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Gominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Direct Submission
Submitted (02-JaN-1989) Shibuya M., Institute of MedfCEl Science,
University of Tokyo, 4-6-1 Shirokane-dai, Minato-ku, Tokyo 108,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /product-"vascular endothelial growth factor receptor"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   X51602
X51602.1 GI:31431
filt gene; fins-related tyrosine kinase gene; tyrosine kinase.
Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3233 CCAAGAGCGACGTGTGGTCTTACGGAGTATTGCTGTGGGAAAICITCTCCTTAGGT 3288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             126 CCAAGAGCGACGTGTGTTACGGAGTATTGCTGTGGGAAAICIICTCCTTAGGT 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 4017;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Shibuya, M., Yamaguchi, S., Yamane, A., Ikeda, T., Tojo, A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HSFLT 7680 bp mRNA linear Human flt mRNA for receptor-related tyrosine kinase.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 114.4; DB 9;
Pred. No. 3.5e-23;
0; Mismatches 1;
                                                                                                 tyrosine kinase"
                                                                                                                                                                       /protein_id="AAC16449.1"
/db_xref="G1:3132831"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CSPPPDYNSVVLYSTPPI"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 503 g
                                                                                                                         /codon_start-1
                                                                                          /note="VEGFR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               38.0%;
1. .4017
/gene="FLT1"
                                                                        /gene="FLT1"
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Shibuya, M.
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Matches 115; Conservative
                                                4017
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VERSION
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JOURNAL
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linear PRI 20-JUN-2002
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Buckley, D., Kibukawa, M., Raymond, C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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ACIO4439 ACO24739
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Kawl, R.K. Olson, W.V. 2 hou, Y., James, R.K., Kouse, G., Wu, Z Saenphimmachak, C., Phelps, K.A., Buckley, D., Kibukawa, M., R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 220965;
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                                                                                                                                                                                                                                                                                                                                                                                                            contig of 53424 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                02408 204978; coniig of 2471 bp in length 04879 204978; gap of 100 bp 04879 213331; coniig of 8553 bp in length 13532 213631; gap of 100 bp 13632 218109; coniig of 4448 bp in length 1810 218209; gap of 100 bp
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219800: contig of 1591 bp in length
19900; gap of 100 bp in length.
220965: contig of 1065 bp in length.
                                          .00 bp
.428 bp in length
                                                                                                      9483: gap of 100 bp
131747: contig of 2264 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   to of 100 bp
contig of 1799 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               gap of 100 bp
3: contig of 9998 bp in length
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       127855: contig of 5921 bp in leagth
                                                                                                                        34455: contig of 2039 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                               9151: gap of 100 bp | 189476: contig of 325 bp in length 9576: gap of 100 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1573: gap of 100 bp
202307: contig of 734 bp in length
2407: gap of 100 bp
                                                                                                                                                                                                                                                                                                                                         contig of 972 bp in length
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llarity 54.7%; Pred. No. 3.4e-20;
Conservative 0; Mismatches 6;
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                                                                   29383: contig of 1428
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/db_xref="taxon:9606"
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                                              gap or
                                                                                                                                                                                                                                                                                                                    gap of
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AC104439.2 GI:21490240
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Direct Submission
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29484 1317
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Best Local Similarity
Matches 108: Conserv
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AUTHORS
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KEYWORDS
SOURCE
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D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        On Apr 5, 2001 this sequence version replaced gi::3548633.
The sequence is a consensus sequence of clone RP4-787C23 (1-140400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          8448-42160 bp Contig 5: 42261-55059 bp Contig 6: 55160-61578 bp
                                                                                                                                                                  the transcriptional map of the common eliminated region 1 (C3CER1)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catàrrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contig
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                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (01-APR-2001) Kiss H., Microbiology and Iumorbiology
Center (MTC), Karolinska Institute, Box 280, Stockholm, S-17177,
                                                                                                      Kiss, H., Yang, Y., Kiss, C., Andersson, K., Klein, G., Imreh, S. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The sequencing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -11731 bp Contig 2: 11832-26218 bp Contig 3: 26319-28347 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           clone RP6-32g23 (31212-220965 bp), clone RP6-146e1 (partially.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              n order and the gaps between them are represented by 100 Ns.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have provided by the submittor.

This sequence will be replaced
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     by the finished sequence as soon as it is available and the accession number will be preserved.

1 11731: contig of 11731 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            35628-189051 bp Contig 18: 189152-189476 bp Contig 19: 89577-191375 bp
contig 20: 191476-201473 bp Contig 21: 201574-202307 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             27956-129383 bp Contig 13: 129484-131747 bp Contig 14: 31848-132316 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   02408-204878 bp Contig 23: 204979-213531 bp Contig 24: 13632-218109 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             17756-118727 bp
contig 10: 118828-121834 bp Contig 11: 121935-127855 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ontig 15: 132417-134455 bp Contig 16: 134556-135527 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               contig 25: 218210-219800 bp Contig 26: 219901-220965 bp. NOTE: This is a 'working draft' sequence. It currently consists of 26 contigs. Gaps between the contigs are represented as runs of N. The order of the pieces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ontig
: 61679-97342 bp Contig 8: 97443-117655 bp Contig 9:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        11732 11831: gap of 100 bp 11832 26218: contig of 14387 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               47: gap of 100 bp 42160: contig of 13713 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              60: gap of 200 bp 55059: contig of 12699 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1579 61678: gap of 100 bp
1679 97342: contig of 35664 bp in length
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97443 117655: contig of 20213 bp in length
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26319 28347: contig of 2029 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 117656 117755: gap of 100 bp 117756 118727: contig of 972 bp in length 118728 118827: gap of 100 bp 118828 121837: contig of 3007 bp in length 121835 121934: gap of 100 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5060 55159; gap of 100 bp
5160 61578; contig of 6419 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1-6800 bp)
and clone RP6-188gll (partially, 1-108303 bp).
                                                                                                                                                                                                                                  . Hum. Genet. 10 (1), 52-61 (2002)
                                                                                                                                                                                                                                                                                                                                     (bases 1 to 220965)
                                                                                                                                                                                                                                                                                                                                                                                                        Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2161 42360:
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TITLE
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Gaps

TOTIE	1	6382	6410	2067	2160	9	<860
	Box 352145, Seattle, WA 98195, USA	C 1.2	0001	3102	0.400		6
REFERENCE	3 (bases 1 to 197279)	777	000	040/	7.94.0	75/7	2803
AUTHORS	Kaul, R.K., Olson, M.V., Zhou, Y., James, R.A., Rouse, G., Wu, Z., Saponchimmachal, C. Dholyo, Y. A. Buchlar, R. Williams, C.	449	<800	3734	3895	5376	5324
	and Haugen, E.D.	2602	2763	TEEL	1303	2000	2479
TITLE			1	* 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	TOC T	C	19/14
JOURNAL	Submitted (20-JUN-2002) Genome Center, University of Washington, Box 352145, Seattle, WA 98195, USA	2590	2617	2287	2309	823	835
, COMMENT	On Jun 20, 2002 this sequence version replaced gi:17466621.	8313	8251	1814	1518	1962	2002
	Center: University of Washington Genome Center	1714	1683	1 7	000	0000	1996
		1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	2	160	0	0067	40.67
	web sire: http://www.genome.washington.edu Contact: uwgchtgs@u.washington.edu	9823	9472	5477	5348	1484	1478
	Drafting Center: WGSSC	516	<800	305	<800	1005	995
	Center project name: chr-3	8587	8291	25245	25541	1181	1171
,	Center Clone name: RPII-793E15 (bc0564)	1 1 1 4	i c	1 (1 1 1	0
	52% of reads	Q##/	1 20 T	80 I I I I I I I I I I I I I I I I I I I	4121	18560	19002
	Sequencing vector: plasmid; LO8752; 48% of reads Chemistry: Dve-terminator ET: 94% of reads	2088	2075	1633	1598	3603	3579
	Chemistry: Dye-terminator Big Dye; 6% of reads Assembly program: Dhran, parsion 0 000116	2509	2617	631	<800	4943	5076
	Consensus quality: 197168 bases at least Q40	3519	3501	0.5	<80.0	95.0E	1241
	Consensus quality: 197255 bases at least 030 Consensus quality: 197275 bases at least 020	1 (1 1 6			
	Insert size: 197279; sum-of-contigs	97	<800	402	<800	8.533	19 19 19 19 19 19 19 19 19 19 19 19 19 1
	Quality coverage: 8.2x in Q20 bases; sum-of-contigs	9 1 5	68.6	3350	3490	1621	1615
	Overlapping Sequences: 5': RP11-91E8 (UWGC:bc0216) AC026349	80 1	<800	4577	4515	6827	0069
	3'; CTD-2563A18 (UWGC:bc0730)	6705	6410	1229	1183	64	<800
٠	Sequence Quality Assessment:	1383	1376	4221	4331	16418	16263
	This entry has been annotated with sequence quality estimates computed by the Phrap assembly program.	0.000	15030	11 0		1	
	All manually edited bases have been reduced to quality zero.	0	7 20 7 A	3980	4121	3361	3241
		1876	1877	2548	2497	872	88.1
	Base-by-base quality values are not generally visible from the GenBank flat file format but are available as part	4169	4068	674	<800	4220	4193
	of this entry's ASN.1 file.	1674	1683	2332	2305	2848	2803
	This sequence was finished as follows unless otherwise moted:	52	<800	11445	11045	2283	2318
	alternate chemistry or covered by high quality data (i.e., Phred	5227	5082	5692	5632	3211	3241
	problems, such as compressions and repeats; all regions were covered by at least one plasmid subclame or more than one bits	15464	15829	1385	1414	4615	4632
		14333	14296	809	<800	6823	0969
	Sequence Validation: This sequence has been validated by Multiple Complete Diggs	1026	1026	3530	3895	886	881
	fingerprinting. Comparison of the experimentally derived digest fragments with sequence-predicted fragments is given below	645	<800	1465	1414	2032	2002
	The electronically-digested sequence consists of both insert and usert in order to account the contract of the	6621	6410	2382	2497	8680	8661
	vector, in older to accurately represent the entire circular BAC. Small fragments below a variable cutoff (approximately 400-800 bp) are not resolved in the fingerprint and hards do not somes.	8413	8251	747	<800	5163	5076
	in the table. There are no significant remaining discrepancies between the experimental and oradiciant remaining discrepancies.	1401	1376	1951	2012	1547	1478
	7	1512	1471	642	<800	7058	0069
		5801	5644	21060	21003	1647	1615
*	Sequencial to the contract of	3256	3278	3700	3666	2753	2803
		1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	3501	1221) () (
	2687 2617 8949 8586 8696 8661	D 3 4 6 7 7 8 10 10 10 10 10 10 10 10 10 10 10 10 10	TOOS	1321	130T	162	008>
		2738	2763	10705	10502	1078	1093

JOURNAL Oncogene 9 (9), 2683-2650 (1994) MEDDINE 9438623 REFERENCE 2 (bases 1 to 4734) AUTHORS Shibuya.M. JOURNAL Unpublished REFERENCE Shibuya.M. JOURNAL Unpublished AUTHORS Shibuya.M. JOURNAL Unpublished REFERENCE Shibuya.M. JOURNAL ON JOURNAL OF JOKYO, Department of Medical Schace Judya.M. JOURNAL CASA (106-7819) Masabuml Shibuya, Institute of Medical Schace Judya-6425 Location/Qualifiers Location/Cualifiers Loc	SVARENGOVETIAGRSHALSAWARAPEPENEWMAKAPEPERSENGURSEUR KUVTAEDAGOTTILLIKOSKIERITININVKAAFPEPENEWMAKAPEPERSENGURSEUR WUTCTVYGIPOPTIKHLHPCHNHSKERNDFCFGEESFILDSSNIGNRIEGITOR MATCHEGTHKYVATHVADSRTPGSSSCKAARATGOVESTILLUVIN WUSLEDSGITACCARNITYTELITATIVUNATHHEISTSKCKAATTOOFSITLLUVIN WUSLEDSGITACCARNITYTELITATIVUNATHHEISTSKCKAATTOOFSITLLUVIN WASLEDSGITACCARNITYTELITATIVUNATHHEISTSKCKAATTOOFSITLLUVIN WASLEDSGITACCARNITYTELITATIVUNATHHEISTSKCKAATTOOFSITLLUVIN WASLEDSGITACCARNITYTELITATIVUNATHHEISTSKCKAATTOOFSITLLUVIN WASLEDSGITACCARNITYTELITATIVUNATHHEISTSKCKAATTOOFSITLLUVIN AAGVOPAPQITTAKNHKINGOPSGITLGFONSTIFFIERITETIVETYPOPPENTATIVUNATHHEISTSKCKAATTOOFSITLLOV GANSVANGTSDSKSELLITATIVUNATHEIRITATIVUNATHATATIVUNATHATIV
237 800 3128 3317 2156 2173 6715 6823 183 <800	Query Match Bast Local Similarity 91.9%; Pred. No. 18-15; Matches 107; Conservative 0; Mismatches 7; Indels 0; Gaps 0; Matches 107; Conservative 0; Mismatches 7; Indels 0; Gaps 0; QY 68 ACTGACTTCCTCTGAAATGGAGGAGTCTTTTGACAAAATCTACGACC 127

DE

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TSPNYTYLKKEPEDTITPDGGRITWDSRRGFILANATYKEIGLINCEAVNGHLYGIN
YLTHROTNTLDVQIRPPSPVRLLLGGTLVLNCTATTELNTRVQALSWRYPGKAİRKAS
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TVIEGTNKTYSTLVVADSQTPGIYSGRAFNKIGIYERYTVRYFYTDVPNGFHYSLEKMP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /db_xref="SWISS-PROT:P35969"
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TGLYTCRYLPTSTSKKKKAESSIYIFYSDAGSPFIEMHIDIPKLYHMIEGRQLIICRY
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SLEDSGTYACRARNIYTGEDILKKFEVLVRDSEAPHLLQNISDYRYSISOSIILLCQA
RCVPAPQITWLKNNHKIQQEPGILLGPGNSTLFIERVTEEDEGVXRCRSTNQKCAVES
AAYLTVQGTSDKSNLELIILTYTCVAATLEFILLILFIRKLKRSSSEVKTDYLSIIMD
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AVKMLKEGATASEYKALMTELKILTHIGHHLNYVNLLGACTKQGGPLMVIVEYCKYGN
LSNYLKSKRDLFCLNKDAALHWELKKESLEPGLEGGQKPRLDSYSSSSVTSSSFPEDR
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     ROD 07-JUL-1954
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KASMKIDLRIASPRKEAGLSDLPRPSFCFSSCGHIRPVQDDESELGKESCCSPFPDYN
                                                                                                                                                               Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

( Dases 1 to 5482)

Choi.K., Wall.C., Hanratty,R. and Keller.G.

Isolation of a gene encoding a novel receptor tyrosine kinase from differentiated embryonic stem cells

Occogne 9 (4), 1261-1266 (1994)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Direct Submission
Submitted (05-JUL-1994) Choi K., 1400 Jackson St. K501, Denver Co
        linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /product="embryonic receptor kinase"
/protein_id="CAA55311.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /cell_type="embryonic stem cells"
  MKNA
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5482 bp
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /db_xref="GI:510665"
                                                                                                           EmRK2 gene; receptor kinase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  'gene="EmRK2"
                          M.musculus EmRK2 cDNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /gene="EmRK2"
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Choi, K.
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                                                                                                                                        Mus musculus.
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                          DEFINITION
                                                                                                                                                                  ORGANISM
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3412 ATACTGGACTICCCCTAAAATGGATGGCICCTGAATCCAICTITGACAAGGICIACAGGA 3471 126 CCAAGAGCGACGTGTGGTTTACGGAGTATTGCTGTGTGGAAATCTTCTCCTTAGG 180 g ò

0;

Gaps

31.8%; Score 95.8; DB 10; Length 5482; 89.6%; Pred. No. 1.2e-17; Live 0; Mismatches 12; Indels 0;

Matches 103; Conservative

Query Match Best Local Similarity

ORIGIN

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MUSKIKB 605-AUG-1993
Mus musculus receptor tyrosine kinase (FLI) mRNA, complete cds.
107297
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KNYSLEDSGTYACRARNIYTGEDILRKTEVLVKDSAAFLLONLSDYEYSISGSTTLD
COARGVPAROITWFKNIYOOPROILLGFRYTETETTETTETTETTETTET
VESAATLIVOGTSKSNELTITICTOVAALEFWILLIFFRKLKRSSSEVKTDYLSI
IMDPDEVPLDEQCEKLPYDASKWEFARERLIKGKSLGRGAFGKVVQASAFGIKKSPTC
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FAELVEKLGDLLQANYQQDGKDYIPLNAILIRNSSFIYSIPIFSEDLFKDGFADPHFH
SGSSDDVRYVNAFKFWSLERIKIFEELSPNSISMFEDYQLDISILLGSPLIKRFTWIE
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TKDVTEDGAGDYTILLGT RQSRLENKITAILITUWK KQUTSKSVSSLEPPPLYPLGSR
QVLTOTYGOLPPRT TIKHWHPOCHHNHSK BRYDEOT NESSSYLLDPSSNLGNRIESISG
RMTVLEGINKIVSTLVVADSQTPGIYSCRAFNKIGIVERNIKFYTDVPNGFHYSLES
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EDRSVSDVEGDEDYSELSKQPLTMEDLISYSFQVARGMEFLSSRKCIHRDLAARNILL
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AGØILFLKCRGEAAHSWSLPTIVSQEDKRLSIIPFSACGRDNRQFCSTLILDTAQANH
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VISPNVIVILKKFPFDILIPDGQRIIMDSRAGFIIANAIYKEIGLLNCEATVNGHLYQ
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ASTRQRIDRSHSHNNYFHSVLKINNYESRDKGLYTGRVKSGSSFQSFNTSVHVYEKGF
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Finnerty, H., Kelleher, K., Morris, G.E., Bean, K., Merberg, D.M., Kriz, R., Morris, J.G., Sookdeo, H., Turner, K.J. and Wood, C.R. Molecular cloning of murine Fir and First 9330572
93330572
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                                                                                                                                                                                                                                     receptor protein tyrosine kinase.
Mus musculus (strain C57BL/6J, sub_species domesticus) cDNA to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3472 CCAASAGCGATGIGIGGICCTATGGCGIGTIGCIGIGGGAGAICLICICCTIAGG 3526
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/protein_id="AAA46078.1"
/db_xref="G1:293783"
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/db_xref="taxon:10090"
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/strain="C57BL/6J"
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KNYSLEDSGTYACRARNIYTGEDILRKTEVLVRDSEAPHILQNLSDYEVSISGSTTLD
CQARGVPAPQITWFKNNHKIQQEPGIILGFGNSTLFIERVTEEDEGVYRCRATNOKGA
VESAAYLTVQGTSDKSNLELITILTCTCVAATLEWILLTETRKKKSSSEVKTDYLSI
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TRPKASMKIDLRTASKSKEAGLSDLPRPSFCFSSCCHIRPYQDDESELGKESCCSPPP
DYNSVVLYSSPPA
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LWEIFSLGGSPYPGYQMDEDFCŠRLKEGMRMRIPEYAIPEIYQIMLDCWHKDPKERPR
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                                                                                    IMDPDEVPLDEQCERLPYDASKWEFAREKLKIGKSIGRGAFGKYVQASAFGIKKSPPC
RIVAVKMLKEGATASEYKALMTELKILTHIGHHLNVVNLLGACTKQGGPLMVIVEYCK
YGNLSNYLKSKRDLFCLNKDAALHWELKKESLEPGLEQGQKPRLDSVSSSVTSSSFP
EDRSVSDVEGDEDYSEISKQPLTMEDLISYSFQVARGMEFLSSRKCIHRDLAARNILL
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/note="exon15"
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2962, .3050
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331, .1067
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AGQTLELKCRGEBAHSWELPTYVSQEDKRLSTTPPPBACGERDNRQFCSITILDIAGANN
TOTAL PTGYSTELSTSTITIDIAGANN
TSPNYTVLPTGYSTSTSTITIDIAGANN
TSPNYTVPLKKFPFDTLTPDGQRITHWSFRGFIIANATYKEIGLINCEATVNGHLYO
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ASTRORIDRSHSHNNYFHSVLKINNYESRDKGLYTCRVKSGSSFQSFNTSVHVYEKGF
ISVKHRKOPVOETTAGRRSYRLSMKVKAFPSPEIVMLKDGSPATLKSARYLVHGYSLI
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QVLTCTVYGIPRPTITWLMHPCHHNHSKERYDFCTENEESFILDPSSNLGNRIESISQ
RMTVIEGTNKTVSTLVVADSQTPGIYSCRAFNKIGTVERNIKFYVTDVPNGFHVSLEK
                                                                                                                                                                                    ROD 30-JUL-2002
                                                                                                                                                                                                                                                                                           Mus musculus (strain:C57/b) lung cDNA to mRNA, clone_lib:mouse lung
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (31-00T-1996) Kunio Kondo, The Institute of Medical Science, The University of Tokyo, Department of Clinical Oncology; 4-6-1 Shirokanedal, Minato-ku, Toky 108, Japan (Tel:+81-3-5499-5628, Fax:+81-3-5449-5628)
                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Shibuya,M. Genomic attion of the fit-1 gene encoding for Vascular Genomic organization of the fit-1 secentary and provth factor (VEGF) receptor-1 suggests an intimate evolutionary relationship between the 7-1g and the 5-1g tyrosine
                                                                                                                                                                                                                                                                                                                                                                                                                    Finnerty, H., Kelleher, K., Morris, G.E., Bean, K., Merberg, D.M., Kriz, R., Morris, J.C., Sookdeo, H., Turner, K.J. and Wood, C.R. Molecular cloning of murine FLT and FLT4 Oncogene 8 (8), 2293-2298 (1993)
                           Kondo, K., Hiratuka, S., Subbalakshmi, E., Matsushime, H. and
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                                                                                                                                                                                    6275~\mbox{bp} mRNA Mus musculus mRNA for flt-1, complete cds.
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1. 6275
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1. .251
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Gene (1998) In press
3 (bases 1 to 6275)
Kondo,K.
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1 (bases 1 to 666)
Scholz, I.D. and Segar, J.L.
Scholz, I.D. and Segar, J.L.
Submitted (0-FEb-2000) Pediatrics, University of Icwa, 200 Hawkins Drive, Iowa City, 1a 52242, USA
Location/Qualifiers
1. 666
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Shibuya,M.
Shibuya,M.
Direct Submission
Submitted (11-JU1-2001) Masabumi Shibuya, University of Tokyo,
Institute of Medical Science, 4-6-1 Shirokane Jan, Minato-ku, Tokyo
108-8639, Japan (E-mail:shibuyaëlms.u-tokyo.sc.jp,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gallus gallus mRNA linear VRI 26-MAY-2002 Gallus gallus mRNA for vascular endothelial growin factor AB065470
                                                                                                                                                                                                                                                                                                                                                                                                                                                /translation="varameflssrkcihrdlaarnillseknvvkiodeglardiyk
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GKOYIPLNAILITGNSAFIYSIPAFSEDFFQEDISAFKFINSGSSDNVRYVNAFNFMSLE
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                                  MAM 28-MAR-2000
                                                                                                                                                       Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Cetartiodactyla, Ruminantia, Pecora, Bovoidea,
Bovidae, Caprinae, Ovis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gallus gallus tissue_lib;whole embryo mRNA.
Gallus gallus
Eukaryita; Metazoa; Chordata; Craniata; Vertabrata; Euteleostomi;
Archossurina; Avos; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Yamaguchi,S., Iwata,K. and Shibuya,M. Soluble Fit-1 (soluble VESTR-1), a potent natural antianglogenic molecule in mammals, is phylogenetically conserved in avians Blochem. Biophys. Res. Commun. 291 (3), 554-559 (2002)
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                                  linear
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3426. .3537
/number=24
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4254. .6275
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RRKTMLEAVAGRKGYRLEMKVRAFPSPEVTWLKDGLPAARCARYWKRYSILIKDVA
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YSCRYPTSPVKKKRESIVYVFINDISNPFVEMHSDIPKIIHMTVGKEMIIPCRVIAPN
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HRETNTIFDIKLSTPRLVKLLKGDSLAINCTVKAAMNTRVQMTWTYPGEAWKRGSVTQ
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EGATASEYKALMTELKILIHIGHHLNIVNLLGACTKNGGPLMVIVEYCKYGNLSNYLK
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EEDEEDAAELYKLPLTMEDLISYSFQVARGMEFLSSRKCIHRDLAARNILLSENNVVK
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TFKIKPPQRIKTFEELPIKEKLVFNDYQADSGMVLASEELKRFTWTGSKQKWTLFGMX
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5449-5550, Fax:81-3-5449-5425)
Location/Qualifiers
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                                                                                /organism="Gallus gallus"
/db_xref="taxon:9031"
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/qene="vegfr-1"
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humquery@sangar.ac.uk clone requests: clonerequest@sangar.ac.uk
on May 25, 2002 this sequence version replaced gi:2020452.
During sequence assembly data is compared from overlapping clones.
Where differences are found these are annotated as variations
together with a note of the overlapping clone name. Note that the
variation annotation may not be found in the sequence submission
corresponding to the overlapping clone, as we submit sequences with
only a small overlap as described above.
This sequence was finished as follows unless otherwise noted: all
regions were either double-stranded or sequenced with an alternate
chamistry or covered by high quality data (i.e., phred quality >=
30; an attempt was made to resolve all sequencing problems, such
as compressions and repeats; all regions were covered by at least
one plasmid sucolone or more than one All subclone, and the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    assembly was confirmed by restriction digest. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em:, EMBL; Swr; SWISSPROT; Tr:, TREMBL; We:, WORMPEP; Information on the WORMPEP database can be found at
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For further details see http://www.chori.org/bacpac/home.htm
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67.7%; Pred. No. 4.1e-13;
tive 0; Mismatches 54;
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Matches 113, Conservative
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/cgn2_6/ptodata/1/pubpna/USO7_NEW_PUB.seq:*
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/cgn2_6/ptodata/1/pubpna/USO8_PUBGOMB.seq:*
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GenCore version 5.1.3 Copyright (c) 1993 - 2002 Compugen Ltd.
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Sequence 35;

Sequence 1 Sequence 9

Sequence 3, Appli Sequence 7, Appli Sequence 18, Appli Sequence 293, App Sequence 159, App Sequence 15, Appl Sequence 17, Appli Sequence 17, Appl Sequence 17, Appl Sequence 17, Appli Sequence 17, Appli Sequence 19, Appli Sequence 193, Appl Sequence 2503, Apple Sequence 2603, Apple Sequence 10423, Apple Sequence 2503, Apple Sequence 255, Appli Sequence 255, Appli Sequence 255, Appli Sequence 255, Appli Sequence 255, Appli Sequence 255, Appli			·Ω.	
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TITLE OF INVENTION: IOTIPOTENT HEMATOPOIETIC STEM CELL
RECEPTORS AND THEIR LIGANDS
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MEDIUM TYPE: Floppy disk
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Sequence 5, Application US/09919408
Patent No. US20020072077A1
GENERAL INFORMATION:
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SIREET: 180 Varick
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ZIP: 10014
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                                                                                                                                                       Length 5470;
                                                                                                                                                     Score 710; DB 10; Length 5 Pred. No. 5.9e-200; Mismatches 575; Indels
                                                                                                  LOCATION: 286..4386
SEQUENCE DESCRIPTION: SEQ ID NO:
LENGTH: 5470 base pairs
                                                                                                                                                                                   0:
                 TYPE: nucleic acid
STRANDEDNESS: unknown
                                                                                                                                                        33.8%;
65.0%;
                                   TOPOLOGY: unknown MOLECULE TYPE: DNA FEATURE:
                                                                                                                                                                                   Matches 1081; Conservative
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COMPUTER: IBM PC compatible
OPPRAIRS SYSTEM: PC-DOS/MS-DOS
OPPRAIRS SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Batentin Release #1.0, version #1.25
CURRENT APPLICATION DAIA:
APPLICATION NUMBER: US/09/919,408
FILING DAIE: 31-Jul-2001
CLASSIFICATION: CURRING: COMPOGND
PRIOR APPLICATION: CURRING: CURRING: CO/9977,451
FILING DAIE: CURRING: CURRING
                                                                                                                                                                                                                     APPLICATION NUMBER: US PCT/US92/05401
FILING DATE: 26-JUN-1992
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APPLICATION NUMBER: US 07/793,065
FILING DAIE: 15-NOV-1991
APPLICATION NUMBER: US 07/728,913
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TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                FILING DATE: 02-APR-1992
APPLICATION NUMBER: US 07/813,593
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FILING DAIE: 26-JUN-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US 07/679,666
FILING DATE: 02-APR-1991
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FILING DATE: 15-APR-1992
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                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DAIE: 28-JUN-1991
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TELEFAX: 212-645-2054
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STRANDEDNESS: double
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                                        CAACCACAAAATACAACAAGAGCCTGGAATTATTTTAGGACCAGGAAGCAGCACGCTGTT 500
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                                                                                                                                          1698 CATGAGGAIGAGAGCICCIGAGTACICIACICCIGAAAICIAICAGATCAIGCIGGACIG 1757
                                                                                                                                                                                                                                                1758 CIGGCACAGAGACCCAAAAGAAAGGCCAAGAIIIGCAGAAACIIGIGGAAAAACIAGGIGA 1817
                                                                                                                                                                                                                                                                        TGGGTCTCCATACCCAGGAGTACAAATGGATGAGGACTTTTGCAGTCGCCTGAGGGAAGG
                                                            1578 CAGCACCAAGAGGGACGIGIGGICTIACGGAGIAIIGCIGIGGGGAAICIICCICTIAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Lemischka, Ihor R.
IIILE OF INVENTION: TOIIPOIENT HEMATOPOIETIC SIEM CELL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DAIA:
                                                                                                                                                                                                                                                                                                              1818 TITGCTICAAGCAAATGTACAACAGGATGGTAAAGACTACAT 1859
                                                                                                                                                                                                                                                                                                                                3687 CCICCIGCAAGCAAAIGCGCAGCAAGGCAAAGACIAIAI 3728
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RECEPTORS AND THEIR LIGANDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: ImClone Systems Incorporated STREET: 180 Varick Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US 07/206,397
FILING DAIE: 26-JUN-1992
APPLICATION NUMBER: US PCI/US92/05401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LICATION NUMBER: US PCI/US92/02750
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/09/208,786
FILING DAIE: <UNKNOWN>
APPLICATION NUMBER: US/09/021,324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DAIE: 15-NOV-1991
APPLICATION NUMBER: US 07/728,913
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DAIE: <Unknown>
APPLICATION NUMBER: US/07/977.453
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ICATION NUMBER: US 07/813,593
NG DAIE: 24-DEC-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US 07/793,065
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE: 28-JUN-1991
APPLICATION NUMBER: US 07/579,666
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/09/872,136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ICATION NUMBER: TW 81102951
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: 01-Jun-2001
CLASSIFICATION: 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       26-JUN-1992
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                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 5, Application US/09872135
Patent No. US20020119545Al
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STATE: New York COUNTRY: U.S.A. ZIP: 10014
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CITY: New York
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US-09-872-136-5
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Pred. No. 1.7e-199;
0; Mismatches 576;
                                                                                         LEM-3-7P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: Sig_peptide
LOCATION: 208..264
SEQUENCE DESCRIPTION: SEQ ID NO: 5:
                                         NAME: Feit, Irving N.
REGISTRATION NUMBER: 28,601
REGISTRATION NUMBER: LB.
IELECOMMUNICATION INFORMATION:
IELEPANE: 212-645-1405
IELEFAX: 212-645-2054
  02-APR-1991
                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
LENGTH: 5406 base pairs
IYPE: nucleic acid
STRANDEDNESS: double
FILING DATE: 02-APR-199
AITORNEY/AGENT INFORMATION:
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265..4308
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208..4311
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65.08;
                                                                                                                                                                                INFORMATION FOR SEQ ID NO: 5:
                                                                                                                                                                                                                                                                                             TOPOLOGY: linear MOLECULE IYPE: cDNA HYPOTHETICAL: NO
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Matches 1080; Conservative
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                                                                               2730 IGCCIICGGCCAAGIGAIIGAGGCAGGCGTIIGGGAAIIGACAGCGACIIGGAA 2789
                                                                                                                                                                                                           1038 AGCCTGCACCAAGCAAGGAGGGCCTCTGATGGTGATTGTTGAATACTGCAAATATGSAAA 1097
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798 IGCCAGCAAGTGGGAATTTGCCCGGGAGAGACTTAAACTGGGCAAATCACTTGGAAGAGG 857
                                                                                                                          918 GACTGTGGGTGTGAAAATGCTGAAAGASGGGCCACGGCCAGCGAGTACAAAGCTCTGNT 977
                  858 GGCTTTIGGAAAAGTGGTTCAAGCATCAGCATITGGCATTAAGAAATCACCTACGTCCC
                                                                                                                                                                                        978 GACTGAGCTAAAAICTIGACCCACATIGGCCACCAICIGAACGIGGITAACCIGCTSS
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                                                                                                                                                                                                                                 Isai, Siao Ping
Wood, William I.
JILLE OF INVENIDO: PROTEIN TYROSINE KINASE AGONIST ANTIBODIES
NUMBER OF SEQUENCES: 45
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MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IRW PC compatable
OPETATING SYSTEM: PC-DOS/MS-DOS
SOFIWARE: WinPatin (Genentech)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity 58.78; Score 541.6; DB 10; Similarity 58.78; Pred. No. 4.6e-150; bl: Conservative 0; Mismatches 679;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/982,610
FILING DATE: 17-0ct-2001
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                     STREET: 460 Point San Bruno Blvd CITY: South San Francisco STAIE: California
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APPLICATION NUMBER: 08/446,648
FILLING DAIE: 1996-MAY-23
APPLICATION NUMBER: 08/222516
FILLING DAIE: 04-APR-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Lee, Wendy M.
REGISTRATION NUMBER: 40,378
                                             Sequence 31, Application US/09982610
Patent No. US20020146420A1
GENERAL INFORMATION:
                                                                                                                Genentech, Inc.
Bennett, Brian D.
Goeddel, David
Lee, James M.
Matthews, William
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     [ELEPHONE: 415/225-1994
                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IYPE: Nucleic Acid
STRANDEDNESS: Single
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RESULT 4
US-09-982-610-31
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MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/982,610
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PRIOR APPLICATION DAIA:
APPLICATION NUMBER: 08/446,648
FILING DAIE: 1996-MAY-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: 08/222616
FILING DATE: 04-APR-1994
AITORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: Generatech, Inc.
STREDT: 460 Point San Bruno I
CITY: South San Francisco
STATE: California
COUNTRY: USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 45, Application US/09982610 Patent No. US20020146420al GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Lee, James M.
Matthews, William
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Goeddel, David
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Wood, William I
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IELEX: 910/371-7168
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STRANDEDNESS: Single
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                                                DB 10; Length 9108;
                                                                                   12;
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                                               Score 541.6; DB 10;
Pred. No. 7.2e-150;
0; Mismatches 679;
 45
; SEQUENCE DESCRIPTION: SEQ ID NO: US-09-982-610-45
                                               25.8%;
58.7%;
                                                            Rest Local Similarity 58.7 Matches 981; Conservative
                                               Query Match
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                                                                                                                                                                                                                                                               1979 IGASCCGCIGACCAIGGAAGAICIIGICIGCTACAGCIICCAGGIGGCCAGAGGGAIGG 4038
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Rood, William I.
IIIE OF INVENTION: PROTEIN IYROSINE KINASE AGONISI ANTIBODIES
                                                                                                                                                                                                                                     1322 AGGAGCCCATCACTATGGAAGATCTGATTTCTTACAGTTTTCAAGTGGCCAGAGGCATGG
                                                                                                                                                                                                                                                                                                                                       1382 AGIICCIGICIICCAGAAAGIGCAIICAICGGGACCIGGCAGCGAGAAACAIICIIITAI
                                                                                     3859 TCGCCAGGCIGGAICGGAGGGGGCCGGGAGCAGCACAGGGICCICITCGCGGGGITCI
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MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: COORDATE
SOFTWARE: WinPatin (Genentech)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CIIY: South San Francisco
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Matthews, William
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Bennett, Brian D
Goeddel, David
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CORRESPONDENCE ADDRESS:
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: Sequence 17, Application US
: Patent No. US20020146420A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 10; Length 5827;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 282.8; DB 10;
Pred. No. 3.5e-73;
0; Mismatches 172;
                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER: P0821P3PCT TELECOMMUNICATION INFORMATION: TELEPHONE: 415/225-1994
CURRENT APPLICATION DATA:
PAPLICATION NUMBER: US/09/982,610
FILING DATE: 17-Oct-2001
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE DESCRIPTION: SEQ ID NO: 17:
                                                          PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/445,648
FILING DATE: 1996-MAY-23
APPLICATION NUMBER: 08/222616
FILING DATE: 04.APR-1994
                                                                                                                                                                       NAME: Lee, Wendy M.
REGISIRATION NUMBER: 40,378
                                                                                                                                                                                                                                                                                                                                    LENGIH: 6827 base pairs
                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
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ilarity 69.2%; Pri
Conservative 0;
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                                                                                                                                                                                                                                                                                                                                               TYPE: Nucleic Acid
STRANDEDNESS: Single
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                                                                                                                                                                                                                                                                            TELEX: 910/371-7168
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Best Local Similarity
Matches 386; Conserva
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RESULT 7 US-09-954-531-1383

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APPLICANT: Weaver, Zoe
IIILE OF INVENTION: Process for identifying Anti-Cancer Therapeutic Agents Using C
IIILE OF INVENTION: Gene Sets
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                                                                                                                                                                                                                      PRICE APPLICATION NUMBER: US/60/23,133
PRICE APPLICATION NUMBER: US/60/23,133
PRICE APPLICATION NUMBER: US/60/234,009
PRICE APLICATION NUMBER: US/60/234,009
PRICE APPLICATION NUMBER: US/60/234,034
PRICE FILING DATE: 2000-09-20
PRICE FILING DATE: 2000-09-20
PRICE FILING DATE: 2000-09-20
PRICE FILING DATE: 2000-09-22
PRICE APPLICATION NUMBER: US/60/234,567
PRICE APPLICATION NUMBER: US/60/234,567
PRICE FILING DATE: 2000-09-22
                                                                                                                                                 FILE REFERENCE: 689290-77
CURRENT APPLICATION NUMBER: US/09/954,531
1383, Application US/09954531, US20020165180A1
                                                                                                                                                                                                           2002-05-02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQ ID NOS: 1392
SCHTWARE: PatentIn version 3.0
SEQ ID NO 1383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches 595; Conservative
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                                                                                                                                                                                                           CURRENT FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
                      Patent No. US2002016
GENERAL INFORMATION:
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1927 GCCCTCATGICTGAACTCAAAGTCCTGAGTTACCTIGGTAATCACATGAATATTGTGAAT 19-5
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                                                                                                                                                                        2044 TAIGGIGALCITITGAATITTTTGAGAAGAAAACGTGATTCATTTATTTGTTCAAAGCAG 2:
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                                                                1030 CIGCIGGGAGCCIGCACCAAGGAGGGCCICIGAIGGIGAIIGIIGAAIACIGCAAA 📭
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ADDRESSEE: ImClone Systems Incorporated
STREET: 180 Varick Street
CIIY: New York
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IIILE OF INVENTION: TOTIPOTENT
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Patent No. US20020072077A1
GENERAL INFORMATION:
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Pred. No. 3.4e-55;
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PRIOR PILING DATE: 2000-09-28
PRIOR FILING DATE: 2000-09-28
PRIOR PELICATION NUMBER: US/60/236,034
PRIOR FILING DATE: 2000-09-28
PRIOR PELICATION NUMBER: US/60/236,111
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TITLE OF INVENTION: Cancer Gene Determinati
TITLE OF INVENTION: Sets
FILE REFERENCE: 68299-72
CURRENT APPLICATION NUMBER: US/09/967,768A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 277, Application US/09967768A Patent No. US20020150877A1 GENERAL INFORMATION:
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Best Local Similarity
Matches 595; Conserv
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US-09-967-768A-277
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Patent No. US20020119545A1
GENERAL INPORMATION:
APPLICANT: Lemischka, Ihor R.
TITLE OF INVENTION: TOTIFOTENT HEMATOPOLETIC STEM CELL
RECEPTORS AND THEIR LIGANDS
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                                                                                                                           MEDIUM IYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
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Pred. No. 1.9e-63;
                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE: CORNONS
APPLICATION NUMBER: 05 07/906,397
FILING DATE: 26-JUN-1992
APPLICATION NUMBER: US PCT/US92/05401
FILING DATE: 26-JUN-1902
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APPLICATION NUMBER: US 07/813,593
FILING DATE: 24-DEC-1991
APPLICATION NUMBER: US,07/793,065
FITTING DATE: 15-NOV-1991
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REFERENCE/DOCKET NUMBER: LEM-3-7P
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-645-1405
                                                                                                                                                                                                                                                         CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/919.408
FILING DATE: 31-Jul-2001

CLASSIFICATION: <Unknown>
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FILING DAIE: 28-JUN-1991
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: 26-JUN-1992
APPLICATION NUMBER: IW 81102951
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| LOCATION: 58.138
| SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-09-919-408-3
                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: 07/977,451
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FILING DAIE: 02-APR-1992
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TYPE: nucleic acid
STRANDEDNESS: double
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139..3036
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SEQUENCE CHARACTERISTICS:
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FRAGMENT TYPE: N-terminal
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58..3039
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Best Local Similarity 55.9%;
Matches 572; Conservative (
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MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
STATE: New York
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DB 10; Length 3501;
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CORRESPONDENCE ADDRESS:
ADDRESSEE: ImClone Systems Incorporated
STREET: 180 Varick Street
                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US 07/906,397
FILING DATE: 26-UN-1992
APPLICATION NUMBER: US PCI/US92/05401
FILING DATE: 26-UN-1992
APPLICATION NUMBER: IW 81102961
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE: 15-APR-1992
APPLICATION NUMBER: US PCI/US92/02750
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE: 28-JUN-1991
APPLICATION NUMBER: US 07/679,666
TORNEY/AGENT INFORMATION:
NAME: Felt, Irving N.
REGISTRATION NUMBER: 28,601
                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US/09/208,786
FILING DAIE: <Unknown>
APPLICATION NUMBER: US/09/021,324
                                                                                                                                                                                                                                                APPLICATION NUMBER: US/09/872.136
FILING DATE: 01-Jun-2001
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE: 24-DEC-1991
APPLICATION NUMBER: US 07/793,055
FILING DATE: 15-NOV-1991
                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US/07/977,451
FILING DATE: 1992-11-19
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APPLICATION NUMBER: US 07/813,593
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SEQUENCE DESCRIPTION: SEQ ID NO: 3:
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                                                                                                                                                        MEDIUM TYPE: Floppy disk
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139..3035
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SEQUENCE CHARACIERISTICS:
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SIRANDEDNESS: double
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58..3039
                                                                                      COUNTRY: U.S.A.
ZIP: 10014
COMPUTER READABLE FORM:
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Best Local Similarity 55.9°
Matches 572, Conservative
                                                          CITY: New York
STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear
MOLECULE TYPE: CDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE:
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ICIGAIGACTGAGCIAAAAICTIGACCCACATTGGCCACCATCTGAACGTGGTIAACCT 1031
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                                                                                                                                                                                                                                                                                                          GCIGGGGGCGIGCACACTGICAGGA---CCAATITACITGATITITGAATACTGTIGCTA 2144
                                                                                                                                                                                                                                                                                                                                                                     1248 IGCGAGCICCGGCITICAGGAAGAIAAAAGICIGAGIGAIGTIGAGGAAGAAGAGGAIIC 1307
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                                                     852 AAGAGGGGTITIGGAAAAGTGGTTCAAGCATCAGCATTTGGCATTAAGAAATCACCTAC 911
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                                                                                                                            GIGCCGGACIGIGGCTGIGAAAIGCIGAAAGAGGGGGCCACGGCCAGCGAGTACAAAGC
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2031 GCIGGGGGGGTGCACACTGTCAGGA---CCAAITIACTTGAIITITGAATACTGITGCTA 2087
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           852 AAGAGGGCTTTTGGAAAAGTGGTTCAAGCATCAGCATTTGGCATTAAGAAATCACCTAC 911
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      912 GIGCCGGACTGIGGCTGIGAAAAIGCIGAAAGAGGGGGCCACGGCCAGGCGAGIACAAAGC 971
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              792 TIATGAIGCCAGCAAGIGGGAGTIIGCCCGGGAGAGTIAAACIGGGCAAAICACIIGG 851
                                                                                                                                                                                                         TITLE OF INVENTION: PROTEIN TYROSINE KINASE AGONIST ANTIBODIES NUMBER OF SEQUENCES: 45 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 10; Length 3120;
                                                                                                                                                                                                                                                                                                                                                                                                      MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
11.8%; Score 247.8; DB 10;
Best Local Similarity 55.8%; Pred. No. 5.3e-63;
Matches 571; Conservative 0; Mismatches 422;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
NAME: Lee, Wendy M.
REGISTRATION NUMBER: 40,378
REFERENCE/DOCKET NUMBER: P0821P3PCT
                                                                                                                                                                                                                                                                                                                                                                                                                                          OPERAIING SYSIEM: PC_DOS/MS-DOS
SOFTWARE: WinPatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/982,610
FILLING DATE: 17-Oct-2001
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Brunc Blvd
CITY: South San Francisco
STAIE: Callifornia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DAIA:
APPLICATION NUMBER: 08/446,648
FILING DAIE: 1996-MAY-23
APPLICATION NUMBER: 08/222616
FILING DAIE: 04-APR-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: Linear SEQUENCE DESCRIPTION: SEQ ID NO: 22:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-1994
                Sequence 22, Application US/09982610
Patent No. US200200146420al
GENERAL INFORMATION:
APPLICANT: Genentech, Inc.
                                                                                                                                  Lee, James M.
Matthews, William
Tsai, Siao Ping
Wood, William I.
                                                                         Genentech, Inc.
Bennett, Brian D.
Goeddel, David
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 3120 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: 415/952-9881
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: Nucleic Acid
STRANDEDNESS: Single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO: 22: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                             ZIP: 94080
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEX: 910/37
                                                                                                                                                                                                                                                                                                                                               COUNTRY: USA
US-09-982-610-22
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1190 CAGGCCIGGAACAAGGCAAGAAACCAAGACIAGAIAGCGICACCAGCAGCGAAAGCII-- 1247
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1368 GCCCAGAGGCAIGGAGTICCTGTCTTCCAGAAAGTGCATTCATCGGGACCTGGCAGCGAG 1427
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1428 AAACAIIČITITAICTGAGAACAACGIGGIGAAGAITTGIGAITITGGCCTIGCCCGGGA 1487
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1488 IAITIATAAGAACCCCGAITATGTGAGAAAAGGAGATACTCGACTICCTCTGAAATGGAI 1547
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2505 TATCATGAGTGATTCCAACTATGTTGTCAGGGCCAATGCCCGTCTGCCTGTAAAATGGAT 2564
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1548 GGCICCCGAAICTAICTITGACAAAAICTACAGCACCAAGAGGGACGIGIGGICTTACGG 1607
                                                                                                                                                                                                                                                                                                                                                2268 IGGGAATICATITCACTCIGAAGAIGAAATIGAATAIGAAAACCAAAAAAGGCIGGAGA 2327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1328 AGAGGAGTIGAATGIGC---TIACATITGAAGATCTTCTTTGCTTTGCATATCAAGT 2384
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2565 GGCCCCCGAAAGCCIGIIIGAAGGCAICTACACCAITAAGAGTGAIGTCIGGICAIAIGG 2624
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2685 IGCTAACTICÍACAAACTGATICAAAATGGATTTAAAATGGATCAGCCATTTTATGCTAC 2744
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2625 AATATTACTGTGGGAAAATCTTCTCACTJGGTGTGAATCCTTACCTGGCATJCCGGJTGA 2684
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IILE OF INVENTION: Method for identifying substances which positively
IILE OF INVENTION: influence inflammatory conditions of chronic
IILE OF INVENTION: inflammatory airway diseases
FILE REFERENCE: 082_00n
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1308 IGACGGIIICIACAAGGAGCCCAICACIAIGGAAGAICIGAITICITACAGIIITCAAGI
1092 IGGAAATCICICCAACIACCICAAGAGCAAACGIG-----
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CURRENT FILINS DATE: 2001-08-31
PRIOR APPLICATION NUMBER: UK 0021484.1
PRIOR FILING DATE: 2000-09-01
NUMBER OF SEQ ID NOS: 24
SCHWARE: Patentin Ver. 2.1
SEQ ID NO 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 9, Application US/09944807
Patent No. US20020119494A1
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                                                                                                                                                                                                                                             2020 AAGIGGGAGITCCCCGGAACAACCIGCAGIIIGGIAAGACCCCCGGGAGCTGGAGCCIII 2079
                                                                                                                                                                                                                                                                                                                                                                                                                                                               1140 GCIGIGAAGATGCTGAAGTCCACGGCCCATGCTGATGAGAAGGAGGCCCTCATGTCCGAG 2199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1045 ACCAAGCAAGGAGGCCTCTGATGGTGATTGTTGAATACTGCAAATATGGAAATCTCTCC 1104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1105 AACTACCTCAAGAGCAAACGTGA---CTTATITTTCTCAACAAGGATGCAGCACTACAC 1161
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                                                                                                                                                                                                           805 AAGIGGGAGIIIGCCCGGGAGAGACIIAAACIGGGCAAAICACIIGGAAGAGGGGCIIII 864
                                                                                                                                                                                                                                                                                                                    855 GGAAAAGIGGITCAAGCAICAGCATIIGGCAIIAAGAAAICACCIACGIGCGGACIGIG 924
                                                                                                                                                                                                                                                                                                                                                                                                                                GCTGTGAAAAIGCTGAAAGAGGGGGCCACGGCCAGGGAGTACAAAGCTCTGATGACTGAG
                                                                                                                                                                 9; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1222 GATAGCGTCACCAGCAGAGAAGCTTTGCGAGCTCCGGCTT---TCAGGAAGATAAAAGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2437 AGIGGCIICICCAGCCAGGGIGIGGACACCIAIGIGGAGAIGAGGCCIGICICCACTICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2677 AAGATIGGGGACTICGGGCIGGCIAGGGACAICAIGAAGACICCAACTACATIGICAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2737 GGCAAIGCCCGCCIGCCTGIGAAGIGGAIGGCCCCAGAAGAACAICIIIGACIGIGICIAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        12797 ACGTICAGAGGACGICIGGICCIAIGACATCICICACIIGGG
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                                                                                  6: DB 10; Length 3992;
1e-58;
                                                                                                                                                           0; Mismatches 444; Indels
                                                                                                        11.1%; Score 233.6;
54.3%; Pred. No. 1e-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1759 IGGCACAGAGACCCAAAAGAAAGGCCAAGAII 1790
                                                                                                                      Best Local Similarity 54.3
Matches 539, Conservative
                      ORGANISM: Homo sapiens
                                                US-09-944-807-9
                                                                                                   Query Match
TYPE: DNA
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AL INFORMATION.
APPLICANT: Lemischka, Ihor R.
IIILE OF INVENTION: TOTIPOIENT HEMATOPOIETIC STEM CELL
RECEPTORS AND THEIR LIGANDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENI APPLICATION DAIA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DAIE: CURKNOWN>
FILING DAIE: CURKNOWN>
FILING DAIE: 26-JUN-1992
APPLICATION NUMBER: US PCT/US92/05401
APPLICATION NUMBER: US PCT/US92/05401
FILING DAIE: 26-JUN-1992
APPLICATION NUMBER: US RILO2961
FILING DAIE: 15-APR-1992
APPLICATION NUMBER: US PCT/US92/02750
                                                                                                                                                                                                                                                                                                          ADDRESSEE: Imclone Systems Incorporated SIREEI: 180 Varick Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DAIE: 02-APR-1992
APPLICATION NUMBER: US 07/813,593
FILING DAIE: 24-DEC-1991
APPLICATION NUMBER: US 07/793,065
FILING DAIE: 15-NOV-1991
APPLICATION NUMBER: US 07/728,913
2977 ISSSCCIIGGAGCCCACACAGACCCACTT 3008
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US/09/919,408 FILING DATE: 31-Jul-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DAIE: 28-JUN-1991
APPLICATION NUMBER: US 07/679,666
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER: LEM-3-7P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/977,451
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Feit, Irving N. REGISTRATION NUMBER: 28,601
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM IYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE: 02-APR-1991
                                                                                                                               Sequence 1, Application US/09919408
Patent No. US20020072077al
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IELEPHONE: 212-645-1405
IELEPHONE: 212-645-2054
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACIERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGIH: 3453 base pairs
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112..3006
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IYPE: nucleic acid SIRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FRAGMENT IYPE: N-terminal
                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES: 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear MOLECULE TYPE: CDNA
                                                                                                                                                                                                                                                                                                                                                     CIIY: New York
STAIE: New York
                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                      10014
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LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ANTI-SENSE: NO
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US-09-919-408-1
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TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DAIE: 02-APR-1991
                                                                                                                                                                                                                                                                                                                                                                         Sequence 1, Application US/09872135 Patent No. US20020119545Al GENERAL INFORMATION:
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TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEPHONE: 212-645-1405
TELEFAX: 212-645-2054
INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AITORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STATE: New York COUNTRY: U.S.A. ZIP: 10014 COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
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US-09-872-136-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IIAACCIGCIGGAGCCIGCACCAAGCAAGGAGGCCICIGAIGGIGAIIGIIGAAIACI 1084
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                                                                                                                                                                                                          785 GGCTCCCITAIGAIGCCAGCAAGIGGGAGTIIGCCCGGGAGAGIIAAACTGGGCCAAAI 844
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                                                                                                                                                                    Gaps
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                                                                                                               DB 10; Length 3453;
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                                                                                                             Score 221.5; DB 10;
Pred. No. 3.3e-55;
0; Mismatches 489;
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LACATION: 31..3009
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-919-408-1
                                                                                                          Query Match 10.5%;
Best Local Similarity 53.0%;
Matches 585; Conservative
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1778 AAAGGCCAAGAIIIGCAGAACTIGIGGAAAACIAGGIGAIIIGCIICAAGCAAAIGIAC 1837
                                                                                                                          2834 AGCGGCCAICCTICCCCAACCIGACTICATTITAGGATGICAGCTGGCAGAGGCAGAAG 2893
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IIILE OF INVENTION: TOTIPOIENT HEMATOPOIETIC STEM CELL
RECEPTORS AND THEIR LIGANDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DAIE: 26-JUN-1992
APPLICATION NUMBER: 1W 81102961
FILING DAIE: 15-APR-1992
APPLICATION NUMBER: US PCT/US92/02750
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US PCT/US92/05401
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FILING DAIE: «Unknown»
APPLICATION NUMBER: US/07/977,451
FILING DAIE: 1992-11-19
APPLICATION NUMBER: US 07/906,397
FILING DAIE: 26-JUN-1992
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APPLICATION NUMBER: US 07/793,065
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APPLICATION NUMBER: US 07/728,913
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APPLICATION NUMBER: US 07/679,666
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US 07/813,593
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/872,136
FILING DATE: 01-010-2001
CLASSIFICATION: GUNKDOWN>
PRIOR APPLICATION: DATA:
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                                                                                                                                                                                     1838 AACAGGAIGGIAAAGACIACAICC 1861
                                                                                                                                                                                                                                             2894 AAGCAIGIAICAGAACAICCAICC 2917
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APPLICANT: INUNO, YASUSHI
TILE COF INVENTION: METHODS AND COMPOSITIONS FOR TREATING FIBRCTIC DISEASES
FILE REFERENCE: ERM-104. WITHOUS AND COMPOSITIONS FOR TREATING FIBRCTIC DISEASES
CURRENT APPLICATION NUMBER: US/09/866,510
PRIOR APPLICATION NUMBER: 60/250,747
PRIOR APPLICATION NUMBER: 60/250,747
PRIOR FILING DATE: 2000-12-01
PRIOR FILING DATE: 2000-12-01
PRIOR FILING DATE: 2001-05-07
NUMBER OF SEQ ID NOS: 33
SOFTWARE: PARENTIN VET: 2.1
                                                                                                                                                      TACAAATGGATGAGGACTTTTGCAGTCGCCTGAGGGAAGGCATGAGGATGAGGATCCTG 1717
                 2594 TGAAGIGGAIGGCACCCGAGAGCTTATTTGAAGGGATCTACACAATCAAGAGTGACGTCT 2653
                                                                      GGTCITACGGAGIATIGCIGIGGGAAAICTICCCTTAGGIGGGICTCCCAIACCCAGGAG 1557
                                                                                              2554 GGTCCTACGGCATCCTTCTGTGGGAGTATTTTCACTGGGTGTGAACCTTACCCTGGCA 2713
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Pred. No. 8.7e-53;
0; Mismatches 486;
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Patent No. US20020111304A1
GENERAL INFORMATION:
APPLICANT: KAZLAUSKAS, ANDRIUS
APPLICANT: IKUNO, YASUSHI
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Best Local Similarity 51.6%;
Matches 621; Conservative (
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                                                                                                                                                                                                                                                                                                                                                                                                           785 GGCTCCCTIATGAIGCCAGCAAGIGGGAGIIIGCCCGGGAGAGACIIAAACIGGGCAAAI 844
                                                                                                                                                                                                                                                                                                                                                                             30; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          845 CACTIGGAAGAGGGGCTTTTGGAAAAGTGGTTCAAGCATCAGCATTTGGCATTAAGAAAT
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                                                                                                                                                                                                                                                                                                                                DB 10; Length 3453;
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                                                                                                                                                                                                                                                                                                                             Score 221.5; DB 10;
Pred. No. 3.3e-55;
0; Mismatches 489;
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                                                                                                                                                                                                                                              SEQUENCE DESCRIPTION: SEQ ID NO: 1:
                                                                                                       mat_peptide
112..3006
                                                                                                                                                                 sig_peptide
                                                            FRAGMENT TYPE: N-terminal
                                                                                                                                                                                                                                                                                                                             Query Match 10.5%;
Best Local Similarity 53.0%;
Matches 585; Conservative
MOLECULE TYPE: CD
HYPOTHETICAL: NO
ANTI-SENSE: NO
                                                                                                                                                                                  LOCATION:
                                                                                                                                                                                                                           NAME/KEY:
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1103	2048	11135	2108	1130	2158	1190	2228	1250	(X)	1310	2348	1370	C)	1430	45	1490	2528	155	eo LC	1610	2648	1670	2768	1730	2768	1790	2828	1850	00		
044 CACCAAGCAAGGAGGGCTCTGATGGGAATTGTTGAATACTGCAAATATGGAAA	92 CACCAAGTCAGGCCCCATTTACATCATCACAGAGTATTGCTTCTAT	4 CAACTACCICAA-	2049 CAACTAITIGCAIAAGAAIAGGAIAGCIICCIGAGCCACCACCCAGAGAAGCAAAGAA	1116GAGCAAACGTGACTT	2109 AGAGCIGGAIAICIIIGGAIIGAACCCIGCIGAIGAAAGCACACGGAGCAAIGIIAIIII	1131 AIIIIIICCCAACAAGGAIGCAGCACIACACAIGGAGCCIAAGAAAAAAAA	2169 ATCTITTGAAAACAATGGTGACTACATGGACATGAAGGAGGCTGATACTACACAGTAGT	1191 AGGCCTGGAACAAGGCAAGAAACCAAGACTAGAIAGCGTCACCAGCAGCGAAAGCTTTGC	2229 CCCCATGCIAGAAAGGAAGAGGIIICIAAAIAIICCGACATCCAGAGAICACICIAIGA	1251 GAGCTCCGGCTTTCASGAAGATAAAAGTCTGAGTGGATGTTGAGGAAGAGGAGGATTCTGA	2289 ICGICCAGCICAIAIAAGAAGAAAICIAIGIIAGACICAGAAGAACTCCIIIC	1311 CGGITICTACAAGGAGCCCAICACTAIGGAAGAICIGAIIICIIACAGITIICAAGIGGC	2349 AGAIGAIAACICAGAAGGCCIIACTIAITGGAITIGITGAGCTICACCIAICAAGIIGC	1371 CAGAGGCAIGGAGTICCIGICIICCAGAAAGIGCAIICAICGGGACCIGGCAGGAAA	2409 CCGAGGAAIGGAGIIIIIGGCIICAAAAAAIIGIGICCACCGIGAICIGGCIGCIGGCAA	1431 CATICITITATCTGAGAACGTGGTGAAGATTTGTGATTTTGGCCTTGCCCGGGGTAT	2469 CGTCCTCCTGGCACAAGGAAAATTGTGAAATTCTGTGACTITGGCCTGGCC	1491 IIATAAGAACCCCGAITAIGIGAGAAAAGGAGAIACICGACIICCICIGAAAIGGAIGG	2529 CAIGCAICGAACIAIGIGICGAAAGCAGIACCIIICICGCCGGGAAGGGGGGGG	1551 TCCCGAATCTATCITIGACAAAATCTACAGCACCAAGAGCGACGTGTGGTTTACGGAGT	2589 ICCIGAGAGCAICIIIGACAACCICIACAACCACIGAGIGATGICIGGITAIGGGAI	1611 ATTGCTGTGGGAAATCTTCTCCTTAGGTGGGTCTCCGATACCCAGGAGTACAAATGGATGA	2649 TCTGCTCTGGGAGAICTITTCCCTTGGTGGCACCCCTTACCCCGGCATGAIGGTGGAITC	1671 GGACTITIGCAGICGCCICAGGGAAGGCAIGAGGAIGAGAGCICCIGAGIACICIACICC	2709 TACTITCIACATAAGATCAAGAGTGGGTACCGGATGGCCAAGGCTGACGAGGGTACCAG	1731 IGABAICIAICAGAICATGCIGGACTGCIGGCACAGAGACCCAAAAGAAAGGCCAAGAII	2769 IGAAGICIACGAGAICAIGGIGAAAIGCIGGAAACAGIGAGCGGAGAAAGAGAGAG	1791 IGCAGAACIIGIGGAAAACIAGGIGAIIIGCIICAAGCAAAIGIACAACAGGA?GIAA	2829 TIACCACCIGAGISACATIGISGAGAAICISCIGCIGCCIGGACAAIAIAAAAAGAGIIAIGA	1851 AGA 1853	1 i 2889 A.A. 2891
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Search completed: December 8, 2002, 14:45:15 Job time : 200.413 secs

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Am Kiopierspitz 18a D-82152 Martinsried, dermany lists is the 5' sequence of the clone insert. Clone from Neleann, Wolecular Genome Analysis, German Cancer Research Center (DKF2), Email s. whemannédkiz-heidelberg.de; sequenced by LMU (Ludwig Maximilians University, Munich/Germany) within the CDNA sequencing consortium of the German Genome Project.

No sl sequence available.
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Manmalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Blum,H., Barcachs,S., Mewes,H.W., Gasseniuker,J. and Wiemann,S.
ESI (Blum, et al.)
Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1091 AIGGAAAICICTCCAACIACCTCAAGAGCAAACGTGACITAITITIICTCAACAAGGAIG 1150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1031 TGCTGCGAGCCTGCACCAAGCAAGGAGGGCCTCTGATGGTGATTGTTGAATACTGCAAAT 1090
                                                                                                                                                                                                                                                                                                                                                                                                                                     851 GAAGAGGGCTTTTGGAAAAGTGGTTCAAGCATCAGCATTTGGCATTAAGAAATCACCIA 910
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            911 CGTGCCGGACTGTGGCTGTGAAATGCTGAAAGAGGGGGCCACGGCCAGGGAGTACAAAG 970
                                                                  671 ICCIATIAACCCICCIIAICCGAAAAATGAAAAGGICTTCTTCIGAAAIAAAGACTGACT 730
                                                                                                                                                                                                                                                       731 ACCIAICAAITAIAAIGGACCCAGAIGAAGITCCTIIGGAIGAGCAGIGIGAGCGGCTCC 790
697 SCACGCISTITATIGAAAGAGICACGGAAGAGGAIGAAGGCGICTAICACIGCAGACCCA 638
                                             551 CCAACCAGAAGGCCTCTGTG3AAAGTTCAGCATACCTCACTGTTCAAGGAACCTCGGACA 610
                                                                                                                                     611 AGTOTAATOTGGAGOTGALCACTOTAACATGCACOTGTGTGGCTGCGACTOTOTTCTGGC 670
                                                                                                                                                                                                                                                                                                                                                791 CIIAIGAIGCCAGCAAGIGGGAGIIIGCCCGGGAGAGCIIAAACIGGGCAAATCACIIG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1337 GAACAGGGGCTTTTGGGAAAGTGGTCCAGGCATCTGCCTTTGGCATTAAGAAATCACCCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   157 IGCIGGGAGCCTGCACGAAGCAAGGAGGCCTCTGATGGTGATGATGATACTGCAAAT
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KEYWORDS
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                                                                                                                                                                                                                                                                          MI-P-CPI-nzb-m-17-0-UI.SI MI-P-CPI Sus scrofa cDNA clone
MI-P-CPI-nzb-m-17-0-UI 3', mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Tissue Procurement: Dr. Chris Tuggle, Iowa State University CDNA Library preparation: Dr. M. Bento Soares, University of Iowa CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa DNA Sequencing by: Dr. M. Bento Soares, University of Iowa Clone Distribution: Researchers may obtain clones from Research Genetics (www.resgen.com).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 (bases 1 to 697)
Bonaldo,M.F., Lennon,G. and Soares,M.B.
Normalization and subtraction: two approaches to facilitate gene
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                                                                  601 CAGGAAGCTCTGATGATGTCACGATATGTAAAIGCTTTCAAGTTCATGAGCCTGGAAAGA 660
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Molecular Genetics Laboratory, Department of Animal Science
Towa State University
201 Kildee Hall, Ames, IA 50011-3150, USA
Tel: 5152944252
                                               2023 ATCAAAACCTTTGAAGAACTTTTACCGAATGCCACCTCCATGTTTGATGACTACCAGGGC
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Pred. No. 5.1e-151;
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/clone="MI-P-CP1-nzb-m-17-0-UI"
/clone_lib="MI-P-CP1"
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97044477
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
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. 181 c 181 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: cktuggle@iastate.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TAG_LIB=MI-P-CP1
TAG_TISSUE=uterus
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POLYA=Yes.
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89.0%;
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BQ604389/c
                                                                                                                                                                                                                                                                                                                        DEFINITION
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/dev_stage="bolding" |
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Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Eriones, M.R., Nagal, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F. F., Coldman, G. H., Carvalho, A.F., Matsukuma, A., Baiaco, S., Simpson, D.H., Brunstein, A., deolivera, P.S., Bucher, P., Jorgeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This sequence was derived from the FAPESP/LICE Human Cancer Genome Project This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=MK3st2=MR3-GN0186-241155-008-calous=2200-11-24st4=1)
Seq primer: puo.18 forward
High quality sequence stop: 594.
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                                                                                                                                                                                                                                                                         Shotgan sequencing of the human transcriptome with GRF
                                                                                                                                                                                                                                                                                                                                                                  Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute Cancer Research
Rua Froit. Antonio Prudente 109, 4 andar, 01553-016,
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/clone_lib="GN0186"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: asimpson@ludwig.org.br
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    This clone (DKFZp434L0121) is available at the RZPD in Berlin. Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14055 Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.
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Citize 115" "NIBERAL FIO"

(Tissue 179e="whole brain"

(dev_stage="embryo 12.6gc"

(Abb_host="billow (II plage resistant)"

(note="Organ: Brain; Vector: prx-Asc; Site_1: Ecor I;

Site_2: Not I; The library was constructed according,

Bonaldo, Lennon and Soares; Genome Research, 6:791-806,

1996. Denatured RNA was size fractionated on a 1% agarose

gel.First strand cDNA Synthesis was primed with oligo-dI

primer containing a Not I sibe. Double strand cDNA was

size selected according to many size fraction, ligated

with Ecor I adaptor; digested with NoLI and then cloned

directionally inte_prx-Asc vector. The library tag

sequence located between the Not! site and the polyA tail

is CAGCACAGC. This library was dreated for the University

Iowa Brain Anatomy Project (BARP): 'Gene Discovery in the

Developing Mouse Nervous System', seported by National

Institute of Montal Health (NIMH), Hemin Chin, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                 50770907
UI-W-FIO-byw-o-22-0-UI.rl NIH_BMAP_FIO Mus musculus cDNA clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Unpublished (1599)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs rimall.nh.gov
Ilssue Procurement: Dr. Jim Lin, University of Iowa
CDNA Library Preparation: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium.LIN. at:
http://mage.linl.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This clone was contributed by the Brain Molecular Anatomy Project
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
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NIH-WGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (WGC)
AAASAAATTACAATCAGAGATCAGGAAGCACCATACCTCCTGCGAAACCTCAGTGATCAC
                                                                                                                      634 AAAGAAATTACAATCAGAGATCAGGAAGCACCATACCTCCTGGGAAACCTCAGTGATCAC
                                                                                                                                                                   ACASTGGCCATCAGCAGTICCACCACTITAGACTGTCATGGTAA1GGTGTCCCCGAGCCT
                                                                                                                                                                                            S74 ACAGIGGCCATCACCACTACACCTTAGACTGTCATGCTAATGGTGTCCCCGAGCCT
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                                                                                                                                                                                                                                                                                         421 CAGAICACTIGGIIIAAAAACAACCACAAAATACAACAAGAGCCIGGAAI 470
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BQ770907
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/clone="IMAGE:6400365"
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/db_xref="Laxon:9606"
/dlone="CSODIO61V018"
/clone="CSODIO61V018"
/clone="Lb="LTJNFLO06_PL2"
/clone="Lb="LTJNFLO06_PL2"
/clone="Lb="Vector: pcNVSPGR16" is Site_1: Not!; ist strand cDNA was primed with a Not!-oliqo(dT) primer. Five prime end enriched, double-stranded cDNA was digested with Not I and cloned into the Not I and Eco RV sites of the pcNVSPGR16 interferenced by Library was normalized. Library was constructed by Life Technologies. Contact: Feng Ling Life Technologies.
a division of Invitrogen 9800 Medical Center Driver Rockville, Maryland 20650, USA Fax: (1) 301 610 8371
Entry //enillangdifference of MRL:
                                                                                                                                                                                                                                                                                                                               AL575294 LTI_NFL006_PL2 Homo sapiens cDNA clone CS0DI061Y018 3
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                                                                      761 TICCTITIGGATGAGCAGTGTGAGCGGCTCCCTTAIGATGCCAGCAAGTGGGAGIIIGCCC 820
                                                                                             1 TATATCACAGATGTGCCAAATGGGTTTCATGTTAACTTGGAAAAATGCCGACGGAAGGA 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.
Location/Qualifiers
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutele
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Li.M.B., Gruber.C., Jessee.J. and Polayes,D.
Full-length cDNA libraries and normalization
Unpublished (2001)
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AL575294
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/db_xref="taxon:9606"
/clone="CSUDIOGSF20"
/tlssue_Lype="placenta"
/tissue_Lype="placenta"
/note="Vector: pCMVSPORT 6; Site_1: Not1; ist strand cDNA was primed with a Not1-oligo(dT) primer. Five prime end
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Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                      781 GAGCGGCTCCCTTATGATGCCAGCAAGTGGGAGTTTGCCCGGGAGAGACTTAAACTGGGC 840
                                                                                                                                                                                                                                                                                                                                                                                              841 AAATCACTTGGAAGAGGGGCTTTTGGAAAAGTGGTTCAAGCATCAGCATTTGGCATTAAG 900
                                                                                                                                                                                                                                                                                                                                                                                                              AAATCACCTACGTGCCGGACTGTGGCTGTGAAAATGCTGAAAGGGGGGCCACGGCCAGG
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                                                541 TGCAAAGCCACCAACCAGAAGGGCTCTGTGGAAAGTTCAGCATACCTCACTGLTCAAGGA 600
                                                                                                                   601 ACCTCGGACAAGTCTAATCTGGAGCTGATCACTCTAACATGCACCTGTGTGGGCTGCGACT 660
                                                                                                                                       CICITCIGGCICCIATTAACCCICCTTAICCGAAAAAIGAAAAGGICITCITCIGAAAIA 720
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                                                                    4 TGCCGAGCCACCAACCAGAAGGGGCCGTGGAAAGCGCAGCCTCACCTCACCGTGCAAGGA 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: seqref@genoscope.ons.fr, Web : www.genoscope.cns.fr.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                             244 GAACGCCTGCCCTATGATGCCAGCAAGTGGGAGTTTGCACGGAGACACTGAAACTAGGC
                ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 (bases 1 to 1005)
Li.W.B., Gruber.C., Jessee,J. and Polayes,D.
Full-length cDNA libraries and normalization
Unpublished (2001)
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Genoscope - Centre National de Sequencage
Pred. No. 5.5e-117;
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87.6%;
                  Matches 493; Conservative
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Best Local Similarity
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enriched, double-stranded CDNA was digested with Not I and cload into the Not I and Ecc RV siess of the pcMYSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies. Contact: Feng Library was constructed by Life Technologies. Contact: Feng Library was constructed by advision of Invitrogen 5600 Medical Center Drive Rockville, Maryland 20860, USA Fax : (1) 301 610 8371 Pmail : filangilifetech.com URL : http://fulllength.invitrogen.com*
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Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: segrefâgenoscope.cns.fr, Web : www.genoscope.cns.fr.
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Pred. No. 7.4e-115;
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/db_xref="taxon:9606"
/clone="CSODI002Y109"
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This read is a RESEQUENCE of a proviously sequenced mouse clone. This read has been verified (found to hit its original self in the correct orientation)
                                                                                                                                                                                                                     This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1522 GATACTCGACTTCCTCTGAAAIGGATGGCTCCCGAATCIATCTTTGACAAAATCTACAGC 1581
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                                                                                                       Louis, MO 63108
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                       Contact: Marra M/Mouse ESI Project
WashU-HHMI Mouse ESI Project
Washington University School of MedicineP
                                                                                                          4444 Forest Park Parkway, Box 8501, St.
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/dev_stage="adult"
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High quality sequence stop: 410.
Location/Qualifiers
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Chordata; Sciurognathi; Muridae; Murinae;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Massa 1 to 855)
Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
Galsel,S., Kucaba,T., Laoy,M., Le,M., Martin,J., Morris,M.,
Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
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Pred. No. 3e-114;
/clone_lib="LTI_NFL006_PL2"
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A1326556.1 GI:4060985
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99.3%;
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Length 855;

8 others

240

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/note="forgan: testis; Vector: pBiuescriptk (modified pBiuescript KS-): Site_1: BamHI; Site_2: Sall-XhoI (gucgap ); Ollgo-dI primed using primer 5-IIITITITITITITITIVIN.3', size-selected for average insert size 2.2 kb and normalized to ROT 5. This is a primary library enriched for All-Length clones and constructed using the for fall-length clones and constructed using the Cap-Irapper method (Carninol, in preparation). Library constructed by M. Brownstein (NNHH,NEGRI, National Institutes of Health), Note: this is a NHH,MGC Library.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ENKATYOTA: MELAZOA; Chordata; Craniata; Vercebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 606)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: cgapbs-rimail.nih.gov
Tissue Procurement: Miklos Falkovits, M.D., Fh.D.
CDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BI458691
603199829F1 NIH_MGC_97 Homo sapiens cDNA clone IMAGE:5265871 5',
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                                                                                                                                      1104 CAACTACCICAAGAGCAAACGIGACIIATITITITCICAACAAGGAIGCAGCACTACACAI 1163
                                                                                                                                                                                                                              1164 GGAGCCTAAGAAAAAAAAGGAGCCAGGCCTGGAACAAGGCAAGAACCAAGACTAGA 1223
                                             1044 CACCAAGCAAGGAGGCCTCTGATGGTGATTGTTGAATACTGCAAATATGGAAATCTCTC 1103
                                                                                                                                                                                                                                                         Toshiyuki and Piero Carninci (RIKEN)
CDNA ilbrary Arrayed by: The T.M.A.G.E. Consortium (LENL)
CDNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
                                                                                                                                                              241 GOTCAAGAICTIGACCCACAICGGCCACCACTGIGAAIGICGICAACCIGCIGGGAGCCIG 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                     10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Plate: LLAMIG670 row: i column: 08
High quality sequence start: 2
High quality sequence stop: 604.
Location/Qualifiers
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Pred. No. 5.4e-104;
0; Mismatches 10;
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                                                                                                                                                                                                                                                                                                                         1224 INGCSICACCAGCAGAGAAGCIIIGCGAGCI 1255
                                                                                                                                                                                                                                                                                                                                            Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Homo sapiens"
/db_xref="taxon:9606"
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                                                                                                                                                                                 EST 12-MAR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                  Casas, E.,
                                                                                                                                                                                                                                                                                                                                                                                     [ (bases 1 to 512) [Feking, B.A., Rohrer, G.A., Smith, T.P.L., Casas, E. Stoneck, R.T., Heaton, M.P., Grosse, M.M., Bennett, G.A., Læegreid, N.W. Design and use of two pooled tissue normalized cDNA libraries for
                                                                                                                                                                                                                                                                                                                         Sus scrofa
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleosiomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note-"Vector: pCMV SPORT6; Site_1: Not1; Site_2: Sal1; Library made from pooled tissue from day 11, 13, 15, 20, and 30 embryos."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            181 TTCIGTAAAAATGCTGAAAGGGGGCCACCGCCAGCGAGTACAAAGCCCTGATGACTGA 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 AAGTGGGAGTTTGCCCCGGGAGACACTGAAGCTGGGCAAATCACTGGGAAGAGGGGCCTTTT 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          924 GGCTGTGAAAATGCTGAAAGAGGGGGCCACGGCCAGCGAGTACAAAGCTCTGATGACTGA 983
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           745 ATGGACCCAGATGAAGTTCCTTTGGATGAGCAGTGTGAGCGGCFCCCTTATGATGCCAGC 804
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Pred. No. 1.2e-106;
0; Mismatches 53; Indels 1;
                                                                                                                                                      512 bp mRNA linear
BG384715
BJ384715
EST. GI:13309187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Smith TPL
USDA, ARS, US Meat Animal Research Center
Dr. Dav. 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4390
Email: smith@email.marc.usda.gov
                       2062 ATGITTGATGACTACCAGGGCGACAGCAGCACTCTG 2097
                                             540 AIGITHIGH HILL HILL HILL HILLHILL S40 AIGITHGAGGACTAICAGCTGGACACTAGCACTCTG 575
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Fiate: 92 row: A column: 16
Seg primer: ATTTAGGTGACACTATAG.
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/lab_host="DH108"
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Best Local Similarity 89.5%;
Matches 45%; Conservative (
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5; Gaps

Length 606;

EST 21-AUG-2001

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/organism~"Homo sapiens"
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                                                                                                                                            18.48;
84.68;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EST 04-FEB-1597
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AA066758 5104-FEB-195 mm09f03.rl Stratagene mouse diaphragm (*537303) Mus musculus cDNA clone IMAGE:521021 5' similar to 9b:L07297 Mus musculus receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
1 (bases 1 to 561)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
                            1413
                                                                                                                                                       1254
                                                                                           176 AGAAAAAATGGAGCCAGGCCTGGAACAAGGCAAGAACCAAGACTAGATAGGGTCACCAG 1235
                                                                                                                                                                                                                     AAGAGGAGTTCTGACGGTTTCTACAAGGAGCCCATCACTAIGG-AAGAICTGATTTCT 1353
                                                                                                                                                                                                                                                                                                                                               1414 GACCTGGCAGCGAGAAACATTCTTTTATCTGAGAACAACGTGGIGAAGATTTGTGATTTT 1473
                                                                                                                                                                                                                                                     436
                                                                                                                                                                                                                                                                                                                   496
138 AGGGCCTCTGATGGTGATTG-TGAATACTGCAAATATGGAAATCTCTCCAACTACCTCAA 196
                                                                                                            TACAGITTTCAAGTGGCCAGAGGCATGGAGTTCCTGTTTCCAGAAAGTGCATTCATCGG
                                                                                                                                                                                                                                                                                                  CACCGAAAGCTTTGCGAGCTCCGGCTTTCAGGAAGATAAA-AGTCTGAGTGATGTTGAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /clone_lib-"Stratagene mouse diaphragm (#937303)"
/tissue_type="diaphragm"
/de_stage="adult"
/lab_host="SolR (kanamycin resistant)"
                                                                                                                                                                                                                                                                                                                                                                                                             :474 GGCCTTGCCCGGGATATTTATAAGAACCCCGATTATGTGAGAAAAGGAGATA 1525
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
12: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                            WashU-HHMI Mouse EST Project
Washington University School or MedicineP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Seg primer: -28ml3 revl ET from Amersham
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       tyrosine kinase (MOUSE);, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Unpublished (1996)
Contact: Marra M/Mouse EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism-"Mus musculus"
/db_xref-"taxon:10090"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: mouseest@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The WashU-HHMI Mouse EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     High quality sequence stop: 368.
Location/Qualifiers
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
(bases 1 to 927)
                                                                                                                                                                                                                                                                                                                                   1522 GATACTOGACTTCCICTGAAATGGATGGCTCCCGGAATCTATCTTTGACAAAATCTACAGC 1581
                                                                                                                                                                                                                                                                                                                                                                                                                                   1532 ACCAAGAGGGACGIGTGGTCITACGGAGTAITGCTGTGGGAAATCITCTCCTTAGGTGGG 1641
                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 ACCAAGAGGAGIGIGGGGCCAIGGGGGTGTGTGGGGAGAICTICICCTTAGGGGGT 120
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BP 191 91006 EVRY cedex - France
Email: segréfégenoscope.cns.fr, Web : www.genoscope.cns.fr.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  301 CITCAAGCCAACGICCAACAGAIGGGAAAGAIIACAICCCCICAAIGCCAIACIGACI
                                                                                                                                                                                                                                                                                                                                                              Length 561;
                                                                                                                                                                                                                                                                                      Indels
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Full-length cDNA libraries and normalization
Unpublished (2001)
                                                                                                                                                                                                               Score 385.6; DB 9;
Pred, No. 3.3e-98;
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/rissue_rype="retina"
/lab_nost="DHIOB (phage-resistant)"
/lab_nost="Cryan: eye; Vector pCMV-SFORI6; Site_1: Noti;
/site_2: SHI; Cloked unidirectionally; Oligo-dI primed.
Average insert size 3.3 kb. Library enriched for
full-length clones and constructed by Life Technologies.
The: this is a NIE-MGC Library.

195 c. 232 g. 183 L.
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                                                                                                                                                                                                                                                                                                                                                                                                                                       17.8%; Score 374.8; DB 13; Length 835;
69.5%; Pred. No. 4.8e-95;
Live 0; Mismatches 247; Indels 8;
tound through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Plate: LLAM11913 row: e column: 22
                                                                                                          1, .835
/organism="Mus musculus'
                                                                                                                                                                           /clone="IMAGE:5359101"
/clone_lib="NIH_MGC_94"
                                                                                                                                                         /db_xref-"taxon:10090"
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Location/Qualifiers
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                                                                            /note="Vector: proxyspor 6; Site_1: Not!; Ist strand obna, was primed with a Not1-ollgo(dT) primer. Five prime end enriched, double-stranded obna was digested with Not I and enriched, double-stranded obna was digested with Not I and ollowed into the Not I and Eco RV sites of the pcWN350R1 6 vector. Library was normalized. Library was constructed by Life Technologies. Contact: Feng Library was constructed by Life Technologies. Contact: Feng Library land Life Technologies, a division of Invitrogen 8800 Medical Center Drive Rockville, Maryland 20850, USA Fax: (1) 301 610 8371 Fmall: Hisangelifetch.com URL:

http://fulleagh.hinvitrogen.com" 4 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BI731060 835 bp mRNA linear ESI 20-SEP-2031 603351683F1 NIH_MGC_94 Mus musculus cDNA clone IMAGE:5359101 5',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Chordata; Craniata; Vertebrata; Euteleostomi; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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Email: cgapbs-rémail.nih.gov
Tissue Procurement: The Cepko Laboratory
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Parrayed by: The I.M.A.G.E. Consortium (LINL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC close distribution information can be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     318 AGAICAGGAAGCACCATACCTCCTGCGAAACCTCAGTGATCACAGTGGCCATCAGCAG 377
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Pred. No. 9.3e-96;
l; Mismatches, 2;
                    /clone="CSODIO30YL03"
/clone_lib="LTI_NFL006_PL2"
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